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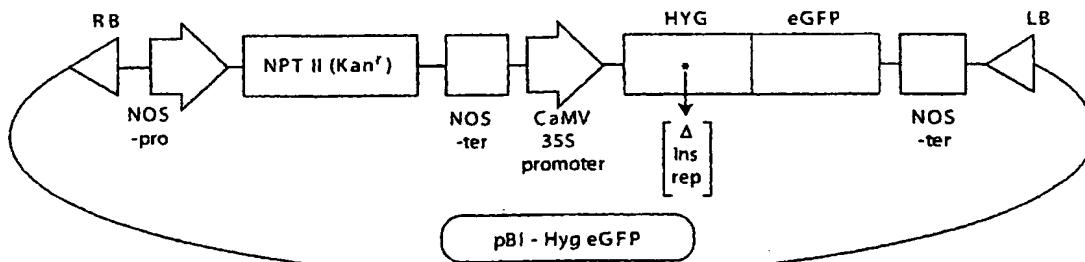
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(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED  
OLIGONUCLEOTIDES



(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclease-resistant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.

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## TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

### Field Of The Invention

The technical field of the invention is oligonucleotide-directed repair or alteration of plant 5 genetic information using novel chemically modified oligonucleotides.

### Background Of The Invention

A number of methods have been developed specifically to alter the genomic information of plants. These methods generally include the use of vectors such as, for example, T-DNA, carrying 10 nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. See, for example, United States Patent 4,459,355 which describes a method for transforming plants with a DNA vector and United States Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene-containing vectors adds one or more exogenous copies 15 of a gene in a usually random fashion at one or more integration sites of the plant's genome at some variable frequency. The introduced gene may be foreign or may be derived from the host plant. Any gene which was originally present in the genome, which may be, for example, a normal allelic variant, mutated, defective, and/or functional copy of the introduced gene, is retained in the genome of the host plant.

20 These methods of gene alteration are problematic in that complications which can compromise the vigor, productivity, yield, etc. of the plant may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. The random nature of this insertion and/or the use of exogenous promoters can also cause the timing, location or strength of expression of the introduced transgene to be inappropriate or unpredictable. Another problem 25 with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, T-DNA ends or other vector remnants, exogenous control sequences required to allow production of the transgene protein, which control sequences may be

exogenous or native to the host plant and/or the transgene, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. In addition, concerns have been raised with consumption, especially by humans, of plants containing such exogenous genetic material.

5 More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant, animal or fungal genomes. See, for example, WO 99/07865 and U.S. Patent 10 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene 15 alteration, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result reduces the utility of such a molecule in methods designed for targeted gene alteration.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. 20 Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of 25 these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such 30 chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

5 Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Similar efforts to target genes by homologous recombination in plants using large fragments of DNA had some success. See Kempin et al., Nature 389:802-803 (1997). However, the efficiency and reproducibility of the published homologous recombination approach in plants has severely limited the widespread use of this method.

10 Earlier experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide rather than larger fragments of DNA, wherein the oligonucleotide had no functional domains other than a region of complementary sequence to the target. See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

15 Oligonucleotides designed for use in the targeted alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for 20 use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to 25 genomic sequences that span the junction between intron sequence and exon sequence.

30 Artificial chromosomes can be useful for the screening purposes identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential *cis*-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large segments of genomic DNA to be cloned and modified (Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat.

Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)). Other vectors also have been developed for the cloning of large segments of genomic DNA, including cosmids, and bacteriophage P1 (Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)). YACs have certain advantages over these alternative large capacity cloning vectors (Burke et al., Science, 236:806-812 (1987)). The maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert size for a YAC.

An alternative to YACs are cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) (Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)). BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. The PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis (Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979)). In addition, BACs have been developed for transformation of plants with high-molecular weight DNA using the T-DNA system (Hamilton, Gene 24:107-116 (1997); Frary & Hamilton, Transgenic Res. 10: 121-132 (2001)).

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

### Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants are identified and the efficiency of alteration is analyzed both *in vitro* using a cell-free extract assay and *in vivo* using a yeast system and a plant system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site specific alteration of DNA is not only useful for studying function of proteins *in vivo*, but it is also useful for creating plants with desired phenotypes, including, for example, environmental stress tolerance, improved nutritional value, herbicide resistance, disease resistance, modified oil production, modified starch production, and altered floral morphology including selective sterility. As described herein,

oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA in cells. The target genomic DNA can be nuclear chromosomal DNA as well as plastid or mitochondrial chromosomal DNA. The target DNA can also be a transgene present in the plant cell, including; for example, a previously introduced T-DNA. For screening purposes, the target plant DNA can also be extrachromosomal DNA present in plant or non-plant cells in various forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing plant DNA can be obtained from a variety of sources, including, e.g., the *Arabidopsis* Biological Resource Center (ABRC) at the Ohio State University, and the Rice Genome Research Program at the MAFF DNA bank in Ibaraki, Japan. The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex. In a more preferred embodiment, the target DNA to be altered is the non-transcribed strand of a transcribed gene of a genomic DNA duplex.

15 The low efficiency of targeted gene alteration obtained using unmodified DNA  
oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction  
mixture or the target cell. Although different modifications are known to have different effects on the  
nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see,  
e.g., Koshkin et al., *J. Am. Chem. Soc.*, 120:13252-3), we have found that it is not possible to predict  
20 which of any particular known modification would be most useful for any given alteration event, including  
for the construction of gene alteration oligonucleotides, because of the interaction of different as yet  
unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been  
developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g.,  
nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that  
25 single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or  
phosphorothioate linkages can enable specific alteration of genetic information at a higher level than  
either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See, for example, copending  
applications United States application no. 60/208,538, United States application no. 60/244,989, United  
States application no. 09/818,875, international application no. PCT/US01/09761 and Gamper et al.,  
30 Nucleic Acids Research 28: 4332-4339 (2000), the disclosures of which are incorporated herein in their  
entirety by reference. We also found that additional nucleic acid analogs which increase the nuclease  
resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-

LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748; Wengel, WO 00/66604; and Jakobsen & Koshkin, WO 01/25478 also allow specific targeted alteration of genetic information.

The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different plants or strains, or testing cells derived from different plants or strains, or plant cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an *in vitro* gene repair assay. Similar results are also observed *in vivo* using yeast, mammalian and plant cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

**25 Detailed Description Of The Invention**

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of plant genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration,

including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity. For example, gene alterations that knockout a particular protein activity can be obtained using oligonucleotides designed to convert a codon in the coding region of the protein to a stop codon, thus prematurely terminating 5 translation of the protein. Oligonucleotides that introduce stop codons in the open-reading-frame of the protein are one embodiment of the invention. Generally, oligonucleotides that introduce stop codons early in the open-reading-frame of the protein are preferred. If the open-reading-frame contains more than one methionine, oligonucleotides that introduce stop codons after the second methionine are 10 preferred. Additionally, if the gene exhibits alternative splice sites, oligonucleotides that introduce stop codons in exons after the alternative splice site are preferred. The following table provides examples of codons that can be converted to stop codons by altering a single oligonucleotide. A skilled artisan could readily identify other codons that can be converted to stop codons by altering one, two or three of the 15 base pairs in a given codon. Similarly, a skilled artisan could readily identify codons that can be converted to stop codons by a frameshift mutations that inserts or deletes one or two base pairs in the open-reading-frame. It is also understood that more than one stop codon can be generated in a single open-reading-frame and that these stop codons can be adjacent in the sequence or separated by intervening codons. Where more than one stop codon is introduced into a single open-reading-frame, such alterations can be generated by a single or multiple oligonucleotides and can be generated simultaneously or by sequential mutagenesis of the target nucleic acid.

	Original codons*	Corresponding stop codon
20	<u>G</u> GA (glycine), <u>A</u> GA (arginine), <u>C</u> GA (arginine), <u>T</u> <u>T</u> A (leucine), <u>T</u> <u>C</u> A (serine), <u>T</u> <u>G</u> T (cysteine), <u>T</u> <u>G</u> G (tryptophan), <u>T</u> <u>G</u> <u>C</u> (cysteine)	TGA
25	<u>A</u> <u>A</u> G (lysine), <u>G</u> <u>A</u> G (glutamate), <u>C</u> <u>A</u> G (glutamine), <u>T</u> <u>T</u> <u>G</u> (leucine), <u>T</u> <u>C</u> G (serine), <u>T</u> <u>G</u> G (tryptophan), <u>T</u> <u>A</u> <u>T</u> (cysteine), <u>T</u> <u>A</u> <u>C</u> (tyrosine)	TAG
	<u>A</u> <u>A</u> A (lysine), <u>G</u> <u>A</u> A (glutamate), <u>C</u> <u>A</u> A (glutamine), <u>T</u> <u>T</u> <u>A</u> (leucine), <u>T</u> <u>C</u> A (serine), <u>T</u> <u>A</u> <u>T</u> (cysteine), <u>T</u> <u>A</u> <u>C</u> (tyrosine)	TAA

\*The amino acid encoded by the original codon is shown in parentheses and the base targeted for alteration to convert the codon to the corresponding stop codon is underlined and in bold

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligo-  
5 nucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain  
10 surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region, are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Preferred oligonucleotides of the invention have at least two modified bases on at least one of the termini, preferably the 3' terminus of the oligonucleotide. Oligonucleotides of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in  
15 the presence of human, animal, plant, fungal (including yeast) proteins and in cells of different types including, for example, plant cells, fungal cells including *S. cerevisiae*, *Ustilago maydis*, *Candida albicans*, and mammalian cells. Particularly preferred are cells and cell extracts derived from plants including, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and  
20 *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as  
25 walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogaea*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyrus*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichorium*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleraceae*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot  
30 (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds,

such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*),  
5. chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g. *tuberosum*) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. *x hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.). Such plant cells can then be used to regenerate whole plants according to methods described herein or any method known in the art. The DNA domain of the oligonucleotides is preferably 10. fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration event(s). On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred 15. embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

20. According to certain embodiments, one or both of the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone (including LNA derivatives and analogs) modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. The oligonucleotides of the invention are, however, single-stranded and are not designed to form a stable 25. internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using 30. modifications other than LNA (including LNA derivatives or analogs), phosphorothioate linkages, or 2'-O-methyl analog incorporation into an oligonucleotide can not yet be predicted because the proteins

involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, oligonucleotides of defined sequence are provided for alteration of genes in particular plants. Provided the teachings of the instant application, one of skill in the art could readily design oligonucleotides to introduce analogous alterations in homologous genes from any plant. Furthermore, in the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. In some embodiments, longer nucleic acids of up to 240 bases which comprise the sequences disclosed herein may be used. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for alteration of particular plant genes contain phosphorothioate linkages, 2'-O-methyl analog or LNA (including LNA derivatives and analogs) or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs (including LNA derivatives and analogs), phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having

phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4 analogs are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration 5 efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl 10 substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods 15 of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substrate 20 molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired 25 the desire change. The oligonucleotides of the invention in different embodiments can alter DNA two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin 30 oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery

which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

5 The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either strand of DNA and can include 10 any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in 15 the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene 20 alteration activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a 25 chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide-dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric 30 RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the

same sequence alteration. Similarly, molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, preferably, using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241) (<http://www.idtdna.com>); this program is available for use on the world wide web at <http://www.idtdna.com/program/oligoanalyzer/> [oligoanalyzer.asp](http://www.idtdna.com/program/oligoanalyzer.asp).

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715, Phone: (608) 258-7420 (<http://www.dnastar.com/products/PrimerSelect.html>).

If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed

strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e. the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

The oligonucleotides of the invention can include more than a single base change. In an oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain, within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target bases only two nucleotides apart are changed together in every case that has been analyzed. The 5 farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the 10 oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

15

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular 20 uptake. For plant cells, biolistic or particle bombardment methods are typically used. According to certain preferred embodiments of the present invention, isolated plant cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Alternatively, plant target DNA may be modified *in vitro* or in another cell type, including for example, yeast or bacterial cells and then introduced 25 into a plant cell as, for example, a T-DNA. Plant cells thus modified may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place *in vivo* following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

The single-stranded, modified oligonucleotides of the present invention have numerous 30 applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention

offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the genetic complement of the organism. Such agents may, for example, be used to develop plants with improved traits by rationally changing the sequence of selected genes in isolated cells and using these 5 modified cells to regenerate whole plants having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated herein by reference. Such plants produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for 10 example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of plants having particular modified or inactivated genes. Altered plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used to introduce molecular markers, including, for example, SNPs, 15 RFLPs, AFLPs and CAPs.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures depending on the target. For example, purified oligonucleotide can be used directly in a standard reaction mixture to introduce alterations into targeted DNA *in vitro* or where cells are the target as a composition adapted for bathing cells in culture or for microinjection into cells in culture. The purified 20 oligonucleotide compositions may also be provided on coated microbeads for biolistic delivery into plant cells. Where necessary, the composition may also include a solubilizing agent. Generally, the ingredients will be supplied either separately or mixed together in single-use form, for example, as a dry, lyophilized powder or water-free concentrate. In general, dosage required for efficient targeted gene alteration will range from about 0.001 to 50,000 µg/kg target tissue, preferably between 1 to 250 µg/kg, 25 and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent 30 such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve

efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein. For biolistic delivery, microbeads are generally coated with resuspended oligonucleotides, which range of oligonucleotide to microbead concentration can be similarly adjusted to improve efficiency as determined using one of the assay methods described herein, starting with about 5 0.05 to 1 microgram of oligonucleotide to 25 microgram of 1.0 micrometer gold beads or similar microcarrier.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an additional reagent or article of manufacture. The additional reagent or article of manufacture may comprise a delivery mechanism, cell extract, a cell, or a plasmid, such as 10 one of those disclosed in the Figures herein, for use in an assay of the invention. Alternatively, the invention includes a kit comprising an isogenic set of cells in which each cell in the kit comprises a different altered amino acid for a target protein encoded by a targeted altered gene within the cell produced according to the methods of the invention.

#### Brief Description Of The Drawings

15 Figure 1. *Flow diagram for the generation of modified single-stranded oligonucleotides.* The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan<sup>s</sup> in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan<sup>s</sup> gene. The numbers 3, 6, 8, 10, 12 and 20 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid 25 indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

30 Figure 2. *Genetic readout system for correction of a point mutation in plasmid pK<sup>s</sup>m4021.* A mutant kanamycin gene harbored in plasmid pK<sup>s</sup>m4021 is the target for correction by oligonucleotides.

The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid pT<sup>S</sup>Δ208 contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. *DNA sequences of representative kan' colonies.* Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(')FIAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a

base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function.

5 Figure 8. *Oligonucleotides for correction of hygromycin resistance gene.* The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

10 Figure 9. *pAURNeo(-)FIAsH plasmid.* This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

15 Figure 10. *pYESHyg(x)eGFP plasmid.* This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

20 Figure 11. *pBI-HygeGFP plasmid.* This plasmid is a construct based on the plasmids pBI101, pBI 101.2, pBI101.3 or pBI 121 available from Clontech in which HygeGFP replaces the beta-glucuronidase gene of the Clontech plasmids. The different Clontech plasmids vary by a reading frame shift relative to the polylinker, or the presence of the Cauliflower mosaic virus promoter.

25 The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

20

#### EXAMPLE 1 Assay Method For Base Alteration And Preferred Oligonucleotide Selection

25 In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK<sup>s</sup>m4021 (Figure 2) or the tetracycline gene of pT<sup>s</sup>Δ208 (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(-)FIAsH (Figure 9), bearing the kan<sup>s</sup> gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase

(kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FlAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FlAsH fusion product (after alteration) or the truncated Neo-/FlAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy.

5 Additional constructs can be made to test additional gene alteration events or for specific use in different expression systems. For example, alternative comparable plant plasmids or integration vectors such as, e.g. those based on T-DNA, can be constructed for stable expression in plant cells according to the disclosures herein. Such constructs would use a plant specific promoter such as, e.g., cauliflower mosaic virus 35S promoter, to replace the promoters directing expression of the neo, hyg or aureobasidinA resistance gene disclosed herein, including for example, in Figures 7B, 9 and 10 herein. Moreover, the green fluorescent protein (GFP) sequence used herein may be modified to increase 10 expression in plant cells such as *Arabidopsis* and the other plants disclosed herein as described in Haseloff et al., Proc. Natl. Acad. Sci. 94(6): 2122-7 (1997), Rouwendal et al. Plant Mol. Biol. 33(6): 989-99 (1997) and Hu et al. FEBS Lett. 369(2-3): 331-4 (1995). Codon usage for optimal expression of GFP in plants results from increasing the frequency of codons with a C or a G in the third position from 32 to about 60%. Specific constructs are disclosed and can be used as follows with such plant specific 15 alterations.

20 We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense 25 termination codon at residue 46. We use pHYGeGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer 30 Hygrepr (5'GACCTATCCACGCCCTCC-3'), HygΔr (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygref (5'-CTGGGATAGGTCTGCAG-3'), HygΔf

(5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGCCTGCGG-3'), respectively to primer HygEGFPr (5'-AAATCACGCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 µg of vector pHYGeGFP and 5 µg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHYGeGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

*Oligonucleotide synthesis and cells.* Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper et al., *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 µg/ml per A<sub>260</sub> unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*recA*).

*Cell-free extracts.* Although this portion of this example is directed to mammalian systems, similar extracts from plants can be prepared as disclosed elsewhere in this application and used as disclosed in this example. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C1271 (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately 2x10<sup>8</sup> cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM MgCl<sub>2</sub>; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000xg. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage.

We then immediately aliquote and freeze the supernatant at -80°C. We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C. We then centrifuge the cultures at 5000xg, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000xg for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000xg for 15 minutes. We then add glycerol to the clarified extract to a concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 µl are used, consisting of 10-30 µg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 µg chimeric double-hairpin oligonucleotide or 0.55 µg single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 µg of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM MgCl<sub>2</sub>, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min. The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 µl H<sub>2</sub>O, and is stored at -20°C. 5 µl of plasmid from the resuspension (~100 ng) was transfected in 20 µl of DH10B cells by electroporation (400 V, 300 µF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 µg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 µl SOC. 200 µl is added undiluted to each of two kanamycin (50 µg/ml) agar plates and 200 µl of a 10<sup>5</sup> dilution is added to an ampicillin (100 µg/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an AccuCount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10<sup>-5</sup> to correct for the amp dilution.

The following procedure can also be used. 5  $\mu$ l of resuspended reaction mixtures (total volume 50  $\mu$ l) are used to transform 20  $\mu$ l aliquots of electro-competent DH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50  $\mu$ g/ml kanamycin or 12  $\mu$ g/ml tetracycline is added for an additional 3 hours.

5 Prior to plating, the bacteria are pelleted and resuspended in 200  $\mu$ l of SOC. 100  $\mu$ l aliquots are plated onto kan or tet agar plates and 100  $\mu$ l of a 10<sup>-4</sup> dilution of the cultures are concurrently plated on agar plates containing 100  $\mu$ g/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads. Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies 10 are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

*Chimeric single-stranded oligonucleotides.* In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan<sup>s</sup> in the HUH7 cell-free extract are presented 15 in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan<sup>s</sup> gene.

Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan<sup>s</sup> system. Alternatively, 20 molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may 25 be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining 30 the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in

the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective 5 gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple 10 experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base 15 changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many 20 phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the exemplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages 25 on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

*Correction of a mutant kanamycin gene in cultured mammalian cells.* Although this portion of this example is directed to cultured mammalian cells, comparable methods may be used using 30 cultured plant cells or protoplasts of those cells from the plant species disclosed herein. The experiments are performed using different eukaryotic cells including plant and mammalian cells, including, for example, 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO<sub>2</sub> in a humidified incubator to a density of 2 x 10<sup>5</sup> cells/ml in an 8 chamber slide (Lab-Tek). After replacing the

regular DMEM with Optimem, the cells are co-transfected with 10  $\mu$ g of plasmid pAURNeo(-)FlAsH and 5  $\mu$ g of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10  $\mu$ g lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan<sup>s</sup> gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that binds to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FlAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FlAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

*Summary of experimental results.* Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid pkan<sup>s</sup>m4021 (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTet $\Delta$ 208. Table 4 illustrates data from repair of the pkan<sup>s</sup>m4021 point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan<sup>r</sup> or tet<sup>r</sup> and fold increases (single strand versus double hairpin) are presented for kan<sup>r</sup> in Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

*Results.* In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion

activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold in certain embodiments when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

5 This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both 10 phenotypic alteration and genetic inheritance can be measured. Plasmid pK<sup>s</sup>m4021 contains a mutation (T→G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of 15 plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of 20 colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

25 The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan<sup>s</sup> mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan<sup>s</sup> mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

30 *Frame shift mutations are repaired.* By using plasmid pT<sup>s</sup>Δ208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is

used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

*Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides.* From a comparison of molecules VII and XI, it is apparent that gene repair is more subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

*Oligonucleotides can target multiple nucleotide alterations within the same template.* The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK<sup>s</sup>m4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence **TTCGATAAGCCTATGCTGACCCGTG** corrects the original mutation present in the kanamycin resistance gene of pK<sup>s</sup>m4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence **TTCGGCTACGACTGGGCACAACAGACAATTGGC** with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK<sup>s</sup>m4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK<sup>s</sup>M4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-

TTGTGCCAGTC**G**T**T**CCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAG**CC**ATTGTCTGTTGTGCCAGTC**G**TAGCCGAA TAGCCTCTCCACCCAAAGCGGCCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-

5 GCTGACAGCCGGAACACGGCGGCATCAGAGCAG**CC**ATTGTCTGTTGTGCCAGTC**G**TAGCCGAAT AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK<sup>m</sup>4021 by monitoring kanamycin 10 resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to determine whether the additional, silent alteration has also been introduced. The results of an analysis 15 are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

20 *Nuclease sensitivity of unmodified DNA oligonucleotide.* Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

*Plant extracts direct repair.* The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, 25 including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract or extracts made from other plant cells disclosed herein. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl;

1.5 mM MgCl<sub>2</sub>; 10 mM DTT; and 10% [v/v] glycerol). Some plant cell-free extracts also include about 1% (w/v) PVP. We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000 x g for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by 5 Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation 10 (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

*Gene repair activity is directed by single-stranded oligonucleotides.*

Oligonucleotide	Plasmid	Extract (ug)	kan' colonies	Fold increase
I	pK <sup>S</sup> m4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
I		20	0	

Plasmid pK<sup>S</sup>m4021 (1 $\mu$ g), the indicated oligonucleotide (1.5  $\mu$ g chimeric oligonucleotide or 0.55  $\mu$ g single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20  $\mu$ g of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan' colonies counted. The data represent the number of kanamycin resistant colonies per 10<sup>6</sup> ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan<sup>r</sup> colonies (second reaction) and in all reactions was calculated using the 20 $\mu$ g sample.

Table II

*Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.*

A. <u>Oligonucleotide</u>	<u>Plasmid</u>	<u>Extract</u>	<u>kan<sup>r</sup> colonies</u>
IX (3S/25G)		HUH7	637
X (6S/25G)		HUH7	836
IX		MEF2 <sup>+</sup>	781
X		MEF2 <sup>+</sup>	676
IX		MEF3 <sup>+</sup>	582
X		MEF3 <sup>+</sup>	530
IX		MEF <sup>++</sup>	332
X		MEF <sup>++</sup>	497
-		MEF2 <sup>+</sup>	10
-		MEF3 <sup>+</sup>	5
-		MEF <sup>++</sup>	14

Chimeric oligonucleotide (1.5 µg) or modified single-stranded oligonucleotide (0.55 µg) was incubated with 1µg of plasmid pK'm4021 and 20µg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 (2<sup>+</sup>) or MSH3 (3<sup>+</sup>) deleted. MEF<sup>++</sup> indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10<sup>6</sup> ampicillin resistant colonies.

Table III

*Frameshift mutation repair is directed by single-stranded oligonucleotides*

Oligonucleotide	Plasmid	Extract	tet <sup>r</sup> colonies
Tet IX (3S/25A; 0.5 µg)	pT <sup>r</sup> Δ208 (1µg)	-	0
Tet IX (0.5 µg)		20µg	0
Tet IX (1.5 µg)			48
Tet IX (2.0 µg)			130
Tet I (chimera; 1.5 µg)			68
			48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide. The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per  $10^6$  ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of pT<sup>r</sup>Δ208. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

*Plant cell-free extracts support gene repair by single-stranded oligonucleotides*

Oligonucleotide	Plasmid	Extract	kan <sup>r</sup> colonies
II (chimera)	pK <sup>S</sup> m4021	30µg Canola	337
IX (3S/25G)		Canola	763
X (6S/25G)		Canola	882
II		<i>Musa</i>	203
IX		<i>Musa</i>	343
X		<i>Musa</i>	746
-		Canola	0
-		<i>Musa</i>	0
IX		- Canola	0
X		- <i>Musa</i>	0

Canola or *Musa* cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 µg) and modified single-stranded oligonucleotides IX and X (0.55µg) were used to correct pK<sup>S</sup>m4021. Total number of kan<sup>r</sup> colonies are present per 10<sup>7</sup> ampicillin resistant colonies and represent an average of four independent experiments.

**Table V**  
*Gene repair activity in cell-free extracts prepared from yeast (*Saccharomyces cerevisiae*)*

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	kan' /amp' x 10 <sup>6</sup>
Wild type	pKan'm4021	1 $\mu$ g		0.36
Wild type		1 $\mu$ g	1 $\mu$ g	0.81
$\Delta$ RADS2				10.72
$\Delta$ RADS2			1 $\mu$ g	17.41
$\Delta$ PMS1		1 $\mu$ g		2.02
$\Delta$ PMS1			1 $\mu$ g	3.23

In this experiment, the kan' gene in pKan'm4021 is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S2SG).

**EXAMPLE 2**  
**Yeast Cell Targeting Assay Method for Base**  
**Alteration and Preferred Oligonucleotide Selection**

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 µg pAUR123 vector DNA, as well as, 10 µg of each pHyg(x)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74 $\alpha$ , is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence.

5 Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2'-O-methylated modified oligonucleotide may be used as a control. Alternatively, oligonucleotides containing one, two, three, four, five, six, eight, ten or more LNA modifications on at least one of the two termini (and preferably the 3' terminus) may be used in different embodiments.

10 *Oligonucleotide synthesis and cells.* We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 MAT $\alpha$  at low copy number under aureobasidin selection. Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare 15 electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD<sub>600</sub> was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml 20 ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120  $\mu$ l 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40  $\mu$ l of cells with 5  $\mu$ g of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes. We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene 25 Pulser apparatus at 1.5 kV, 25  $\mu$ F, 200  $\Omega$  for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We then spread 200  $\mu$ l of this culture on selective plates containing 300  $\mu$ g/ml hygromycin and spread 200  $\mu$ l of a 10<sup>5</sup> dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then 30 count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10<sup>5</sup> aureobasidinA resistant colonies.

*Frameshift mutations are repaired in yeast cells.* We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells

containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction 5 activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in 10 pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-  
15 CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGGTAC**GT**CCTGCGGGTAAATAGCTGCGCCGATG  
GTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-  
CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGGA**T**CCTGCGGGTAAA**C**GCTGCGCCGATG  
GTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-  
CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGGA**T**CCTGCGGGTAAATAGCTGCGCCGA**C**  
20 GTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

*Oligonucleotides targeting the sense strand direct gene correction more efficiently.* We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target 25 sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74 $\alpha$ , with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the 30 synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6  $\mu$ g, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74 $\alpha$  and HygE3T/74).

Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74 $\alpha$  relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation 5 more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

10 *Optimization of oligonucleotide concentration.* To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74 $\alpha$  to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given 15 oligonucleotide. We test the ability of Hyg3T/74 $\alpha$  to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0  $\mu$ g. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in *pAURHYG(ins)GFP* by *HygGG/Rev*, *HygE3T/25* and *HygE3T/74*

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10 <sup>5</sup> )	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μg)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

\* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

*Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.*

Oligonucleotide Tested (5 µg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

Table 9

*Optimization of oligonucleotide concentration in electroporated yeast cells.*

Amount (µg)	Colonies on hygromycin	Colonies on aureobasidin (/10 <sup>5</sup> )	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

### Example 3 Cultured Cell Manipulation

Although disclosure in this example is directed to use of stem cells or human blood cells and microinjection, the microinjection procedures may also be used with cultured plant cells or protoplasts using any plant species, including those disclosed herein. Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either

the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). Lin<sup>-</sup>CD38<sup>-</sup> cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA). Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection.

5 S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 µg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 µg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM; Stem Cell Technologies), 40 µg/ml low-density lipoprotein (LDL; Sigma, St. Louis, MO), 50 mM HEPES buffer and 50 µM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After 10 microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

35 mm dishes are coated overnight at 4° C with 50 µg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are 15 removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 µm to 0.3 µm outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transjector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are fluorescently labeled allow determination of the amount of 20 oligonucleotide delivered to the cells.

For *in vitro* erythropoiesis from Lin<sup>-</sup>CD38<sup>-</sup> cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative 25 capacity and the ability to generate myeloid and erythroid progeny. CD34+ cells can convert a normal A ( $\beta^A$ ) to sickle T ( $\beta^S$ ) mutation in the  $\beta$ -globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

30 Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids,

liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

Biostatic delivery of oligonucleotide into plant cells may be accomplished according to the following method. One milliliter of packed cell volume of plant cell suspensions are subcultured onto 5 plates containing solid medium [with Murashige and Skoog salts from Gibco/BRL, 500 mg/liter Mes, 1 mg/liter thiamin, 100 mg/liter myo-inositol, 180 mg/liter KH<sub>2</sub>PO<sub>4</sub>, 2.21 mg/liter 2,4-dichlorophenoxyacetic acid (2,4-D), and 30 g/liter sucrose (pH 5.7) and having 8 g/liter agar-agar from Sigma added before autoclaving]. By using a helium-driven particle gun such as that from BioRad and following manufacturers 10 directions, oligonucleotides may be introduced to cells after precipitation onto 1 micrometer or comparable gold microcarriers (Bio-Rad). To precipitate onto microcarriers, 35 microliters of a particle suspension (60 mg of microcarriers per ml of 100% ethanol) is transferred to a 1.5 ml microcentrifuge tube, which is agitated on a vortex mixer. Then 40 microliter of resuspended oligonucleotide (60 15 ng/microliter water) is added; then 75 microliter of ice-cold 2.5 M CaCl<sub>2</sub> is added; then 75 microliter of ice-cold 0.1 M spermidine is added. The tube is mixed vigorously or a vortex mixer for 10 min at room 20 temperature. The particles are allowed to settle for 10 min and are centrifuged at 11,750 g for 30 sec. The supernatant is removed and the particles are resuspended in 50 microliter of 100% ethanol. An aliquot of 10 microliter of the resuspended particles are applied to each macro-projectile which is used to bombard each plate once at 900 psi (1 psi = 6.89 kPa) with a gap distance (distance from power source to macroprojectile) of 1 cm and a target distance (distance from microprojectile launch site to target material) of 10 cm.

An alternative method of delivery can be used as follows. Cultured cells are suspended in liquid N6 medium and then plated on a VWR Scientific glass fiber filter. About 0.4 microgram of oligonucleotide are precipitated with 15 microliter of 2.5 mM CaCl<sub>2</sub> and 5 microliter of 0.1 M spermidine onto 25 microgram of 1.0 micrometer gold particles. Microprojectile bombardment is performed by using a Bio-25 Rad PDS-1000 He particle delivery system or comparable machine following manufacturers instructions. Alterations in oligonucleotide concentrations can be employed to determine the optimum concentration of oligonucleotide according to the procedures described herein for any particular oligonucleotide of the invention.

Alternatively, the oligonucleotide of the invention may be delivered to a plant cell by 30 electroporation of a protoplast derived from a plant part. The protoplasts may be formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques such as those in Gallois et al., Methods in Molecular Biology 55: 89-107 by Humana Press. Such conditions for electroporation use

about  $3 \times 10^5$  protoplasts in a total volume of about 0.3 ml with a concentration of oligonucleotide of between 0.6 to 4 microgram per ml.

#### EXAMPLE 4

##### Plant Cells

5           The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific 10 site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon

15           Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

20           For introduction of a T-DNA, including the T-DNA in the plasmid of Figure 11, into a plant cell, *Agrobacterium tumefaciens* is used. These techniques are routine standard techniques known in the art. For example, one method follows. We transform *A. tumefaciens* is transformed by electroporation (using a BioRad Gene Pulser™). Competent *A. tumefaciens* is prepared using a method similar to that of preparing competent *E. coli* by suspending a freshly grown culture three times in ice-cold water and a final resuspension in 10% glycerol. Electroporation conditions are a 0.2 cm gap cuvette at a setting of 25  $\mu$ F, 200  $\Omega$  and 2.5 kV.

25           *A. tumefaciens* containing a plasmid with a T-DNA is then used to introduce the T-DNA into a plant cell using routine standard techniques known in the art. For example, we transform *Arabidopsis* by vacuum infiltration or by dipping flowers in an *Agrobacterium* solution containing a surfactant, e.g. L-77. Seeds are then collected, grown and screened for presence of the T-DNA. Alternatively, *Agrobacterium* can be used to transform callus tissue and the callus tissue can then be used to regenerate transformed plants.

30           All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some

detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

5 **Notes on the tables presented below:**

Each of the following tables presents, for the specified gene, a plurality of mutations that are known to confer a relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the genome according to the present invention.

10 The left-most column identifies each alteration or mutation and the phenotype that the alteration/mutation confers.

15 For most entries, the mutation/alteration is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

20 The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the genome or in cloned DNA including DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

25 All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

30 The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair/altering nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair/alteration. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair/alteration nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

**Example 5**  
**Engineering herbicide resistant plants**

Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new

5 high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

**Table 10**  
**Genome-Altering Oligos Conferring Glyphosate Resistance**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO
5	Glyphosate Resistance EPSPS <i>Arabidopsis thaliana</i> Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTCCTGCCTCCAAGTCTCTATCAAATCGGATCCTGC TTCTCGCTGCTCTGCTGAGGTATATATCAC	4341
		GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT TGATAGAGACTGGAGGCAGGAAGCTTAATAAGACCGGAGATT CTCTAATGGGTTGAAGTACAATCTCCGACGCTT	4342
		GCTTCCTGCCTCCAAGT	4343
		ACTTGGAGGCAGGAAGC	4344
10	Glyphosate Resistance EPSPS <i>Brassica napus</i> Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTCAACCAATCAGAGAAATCTGGGTC TCATTAAGCTACCCGCATCCAATCTCTCAATCGGATCCTCC TTCTGCCGCTCTATCTGAGGTACATATACT	4345
		AGTATATGTACCTCAGATAGAGCGGCAGAAGGAGGATCCGATT GGAGAGAGATTGGATCGGGTAGCTTAATGAGACCCGAGATT CTCTGATTGGTTGAAGCACAATCTCTGAAGCTT	4346
		GCTACCCGCATCCAAT	4347
		ATTTGGATCGGGTAGC	4348
		AGCCCAACGAGATTGTGCTCAACCCATCAAAGATATATCAGGC ACTGTTAAATTGCCCTGCTTCTAAATCCCTTCCAATCGTATTCTCC TTCTGCTGCCCTTCTAAGGGAAGGACTGT	4349
15	Glyphosate Resistance EPSPS 1 <i>Nicotiana tabacum</i> Gly95Ala GGT-GCT	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTAGAACAGGCAATTAAACAGTGCCTGATATATC TTTGATGGGTTGCAGCACAATCTCGTTGGGCT	4350
		ATTGCCCTGCTTCTAAAT	4351
		ATTTAGAACAGGCAAT	4352
		ATTGTTCCCTGGTACGAAATGTCCTCCTGTTGCAATTGTCAGCA AGGGAGGCCTCCCGCAGGGAAAGGTAAGCTCTGGATCAATT AGCAGCCAGTACTGACTGCTCTGCTTATGGC	4353
		GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGA GAGCTTACCTTCCCTCGGGAAAGGCCTCCCTGCTGACAATT GAACAGGAGGACATTCGTACCAAGGAAACAAT	4354
20	Glyphosate Resistance EPSPS 2 <i>Nicotiana tabacum</i> Gly62Ala GGA-GCA	CCTTCCCGCAGGGAAAGG CCTTCCCTCGGGAAAGG	4355 4356
		ATTGTTCCCTGGCACTGACTGCCACCTGTCGTGCAATGGAA TCGGAGGGCTACCTGCTGGCAAGGTCAGCTGTCTGGCTCCATC AGCAGTCAGTACTGAGTGCCTGCTGATGGC	4357
		GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA CAGCTTGACCTTGGCAGCAGGTAGCCCTCCGATTCCATTGACAC GAACAGGTGGCAGTCAGTGCCAGGAAACAAT	4358
25	Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT		
30	Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCTACCTG <u>C</u> GGCAAGG	4359
	CCTTGCC <u>C</u> AGCAGGTAGC	4360
5 Glyphosate Resistance EPSPS <i>Oryza sativa</i> Gly115Ala GGT-GCT	ACTGTTTCC <u>T</u> GGCACTGAATGCCACCTGTCGTGTCAAGGGA ATTGGAGGGACTCCT <u>G</u> CTGGCAAGGTTAAGCTCTGGTTCCAT CAGCAGTCAGTACTTGAGTGCC <u>T</u> GCTGATGGC	4361
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGA GAGCTTAACCTG <u>C</u> CCAGCAGGAAGTCCTCCAATTCCCTGACAC GAACAGGTGGGCATT <u>C</u> AGTGCCAGGAAACAGT	4362
	ACTTCC <u>T</u> GGCAAGG	4363
	CCTTGCC <u>C</u> AGCAGGAAGT	4364
10 Glyphosate Resistance EPSPS <i>Petunia x hybrida</i> Gly93Ala GGC-GCC	AGCCTTCTGAGATAGTGTGCAACCCATTAAAGAGATTCAGGCA CTGTTAAATTGCCT <u>G</u> CTCTAAATCATTATCTAATAGAATTCTCCT TCTTGCTGCCTTATCTGAAGGAACA <u>CT</u> GT	4365
	ACAGTTGTTCC <u>T</u> TCAGATAAGGCAGCAAGAAGGAGAATTCTATT GATAATGATTAGAG <u>G</u> CAGGCAATTAA <u>C</u> AGTGCTGAAATCTCT TTAATGGGTTGCAACACTATCTCAGAAGGCT	4366
	ATTGCCT <u>G</u> CTCTAAAT	4367
	ATTTAGAG <u>G</u> CAGGCAAT	4368
15 Glyphosate Resistance EPSPS <i>Lycopersicon esculentum</i> Gly97Ala GGT-GCT	AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTA CTGTTAAATTACCC <u>G</u> CTTGAAATCCCTTCC <u>A</u> TC <u>G</u> TATTCTCCT TCTTGCTGCC <u>T</u> CT <u>G</u> AGGGGAAGGACTGT	4369
	ACAGTC <u>T</u> CC <u>C</u> TCAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATT <u>C</u> GAAG <u>G</u> GGTAATTAA <u>C</u> AGTACCA <u>CT</u> CATGGGTT	4370
	TTTGATGGGTNCTAGCACAAT <u>CT</u> CATGGGTT	
	ATTACCC <u>G</u> TT <u>C</u> GAAAT	4371
	ATTC <u>G</u> GAAG <u>G</u> GGTAAT	4372
20 Glyphosate Resistance EPSPS <i>Lolium rigidum</i> Gly107Ala GGT-GCT	ATTGTTTCC <u>T</u> GGCACTGACTGCCACCTGTC <u>G</u> KATCAACGGCA TTGGAGGG <u>G</u> TAC <u>C</u> T <u>G</u> CTGGCAAGGTTAAGCTGTCTGGTTCCATC AGCAGCCA <u>A</u> ACTTGAG <u>T</u> CC <u>T</u> GCTGATGGC	4373
	GCCATCAGCAAGGA <u>CT</u> CAAGTATTGGCTGCTGATGGAACCAGA CAGCTTAACCTG <u>C</u> CCAG <u>G</u> CAGGTAG <u>C</u> CC <u>T</u> CCAATGCC <u>T</u> GATCG AACAGGTGGGCAGTCAGTGCC <u>A</u> GGAAACAA <u>T</u>	4374
	GCTACCTG <u>C</u> GGCAAGG	4375
	CCTTGCC <u>C</u> AGCAGGTAGC	4376

**Table 11**  
**Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Ser CCT-TCT	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTAGCA ATCACAGGACAAGTCTCTCGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4377
		AACGCGTTACCTCAACAATCGGAGTCTCTGAAACGCATCTGTAC CAATCATACGACGAGAGACTTGTCCCTGTGATTGCTACAAGAGGAA CACTATCTAACAAACGCATCGGCTAACCGCT	4378
		GACAAGTCTCTCGT	4379
		ACGACGAGAGACTTGT	4380
		AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTAGCA ATCACAGGACAAGTCCAGCGTCGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4381
10	Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAG	AACGCGTTACCTCAACAATCGGAGTCTCTGAAACGCATCTGTAC CAATCATACGACGCTGGACTTGTCCCTGTGATTGCTACAAGAGGAA CACTATCTAACAAACGCATCGGCTAACCGCT	4382
		ACAAGTCCAGCGTC	4383
		TACGACGCTGGACTTGT	4384
		AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTAGCA ATCACAGGACAAGTCCAACGTCGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4385
		AACGCGTTACCTCAACAATCGGAGTCTCTGAAACGCATCTGTAC CAATCATACGACGTTGGACTTGTCCCTGTGATTGCTACAAGAGGAA CACTATCTAACAAACGCATCGGCTAACCGCT	4386
15	Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAA	ACAAGTCCAACGTC	4387
		TACGACGTTGGACTTGT	4388
		GACCTTACCTGTTGGATGTGATTGTCGCACCAAGAACATGTGT TGCCGATGATCCCGAACGGTGGCACTTCAACGATGTACATAACGG AAGGAGATGGCCGGATTAATACTGAGAGAT	4389
		ATCTCTCAGTATTAATCCGGCCATCTCCTCCGTTATGACATCGT TGAAAGTGCCACCGTTCGGGATCATCGGCAACACATGTTCTGGT GCGGACAAATCACATCCAACAGGTAAAGGTC	4390
		GATCCCGAACGGTGGCA	4391
20	Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAC	TGCCACCGTTGGGATC	4392

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTGTCGCACCAAGAACATGTGT TGCCGATGATCCCGAATGGTGGCACTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4393
		ATCTCTCAGTATTAATCCGGCCATCTCCTCCGTTATGACATCGT TGAAAGTGCCACC <u>ATT</u> CGGGATCATCGGCAACACATGTTCTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4394
		GATCCC <u>GAAT</u> GGTGGCA	4395
		TGCCACC <u>ATT</u> CGGGATC	4396
		TCCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCGGATGGTCG CCATCACGGGCCAGGT <u>CT</u> CCGCCATGATCGGCACCGACGC CTTCCAGGAGACGCC <u>CA</u> AGTCGAGGTACCCGCT	4397
10	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT CCGATCATGCGGCCGG <u>AG</u> ACCTGGCCCGT <u>G</u> ATGGCGACCATCG GGACGGAGTCGAGCAGCGC <u>T</u> CGGGAGCGCGGA	4398
		GCCAGGT <u>CT</u> CCGCCGC	4399
		GC <u>GGCGGGAG</u> ACCTGGC	4400
		CCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCGGATGGTCG CATCACGGGCCAGGT <u>CC</u> <u>A</u> CCGCCATGATCGGCACCGACGCC TTCCAGGAGACGCC <u>CA</u> AGTCGAGGTACCCGCTC	4401
		GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGCG <u>T</u> GGACCTGGCCCGT <u>G</u> ATGGCGACCATCG GGACGGAGTCGAGCAGCGC <u>T</u> GGCGAGCGCGG	4402
15	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	CCAGGT <u>CCA</u> ACGCCGCA	4403
		TGCGGC <u>GT</u> GGACCTGG	4404
		CCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCGGATGGTCG CATCACGGGCCAGGT <u>CC</u> <u>A</u> CCGCCATGATCGGCACCGACGCC TTCCAGGAGACGCC <u>CA</u> AGTCGAGGTACCCGCTC	4405
		GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGCG <u>T</u> GGACCTGGCCCGT <u>G</u> ATGGCGACCATC GGGACGGAGTCGAGCAGCGC <u>T</u> GGCGAGCGCGG	4406
		CCAGGT <u>CCA</u> ACGCCGCA	4407
20	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	TGCGGC <u>GT</u> GGACCTGG	4408
		CCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCGGATGGTCG CATCACGGGCCAGGT <u>CC</u> <u>A</u> CCGCCATGATCGGCACCGACGCC TTCCAGGAGACGCC <u>CA</u> AGTCGAGGTACCCGCTC	4409
		GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGCG <u>T</u> GGACCTGGCCCGT <u>G</u> ATGGCGACCATC GGGACGGAGTCGAGCAGCGC <u>T</u> GGCGAGCGCGG	4410
		CCAGGT <u>CCA</u> ACGCCGCA	4407
		TGCGGC <u>GT</u> GGACCTGG	4408
25	Imidazolinone Resistance ALS <i>Oryza sativa</i> Ile627Asn ATT-AAT	GGCCATACTTGTGGATATCATCGTCCCGCACCGAGGAGCATGTGC TGCCTATGATCC <u>CA</u> <u>A</u> GGGGCGCATTCAAGGACATGATCCTGG ATGGT <u>G</u> ATGGCAGGACTGTGTATTAA <u>T</u> CTAT	4409
		ATAGATTAATACACAGTCCTGCCATACCCATCCAGGATCATGTCCT TGAATGCGCCCC <u>CA</u> <u>T</u> GGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATCCAACAA <u>G</u> TATGGCC	4410
		GATCCC <u>AA</u> <u>A</u> GGGGCG	4411
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS	CGCCCCCATTTGGGATC	4412
Zea mays Pro165Ser CCG-TCG	TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT	4413
	TCCAGGAGACGCCATCGTCGAGGTACCCGCT AGCGGGTGACCTCGACGATGGCGTCTCCTGGAAGGCGTCGGT	4414
	GCCAATCATGCGTCGCGACACCTGTCCCGTATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	
	GACAGGTGTCGCGACGC	4415
	GCGTCGCGACACCTGTC	4416
Sulfonylurea Resistance ALS	CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGCAAGCGACGCATGATTGGCACCGACGCCT	4417
Zea mays Pro165Gln CCG-CAG	CCAGGAGACGCCATCGTCGAGGTACCCGCT GAGCGGGTGACCTCGACGATGGCGTCTCCTGGAAGGCGTCGGT	4418
	TGCCAATCATGCGTCGCTGCACCTGTCCCGTATGGCGACCATG	
	GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	
	ACAGGTGCAAGCGACGCA	4419
	TGCCTCGCTGCACCTGT	4420
Imidazolinone Resistance ALS	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAATGGTGGGGCTTCAAGGATATGATCCTGG	4421
Zea mays Ser621Asn AGT-AAT	ATGGTGATGGCAGGACTGTGTACTGATCTAA TTAGATCAGTACACAGTCCTGCCATACCATCCAGGATCATATCCT	4422
	TGAAAGCCCCACCCATTAGGGATCATAGGCAACACATGCTCCTGGT	
	GTGGGACGATTATATCCAAGAGGTACGGCC	
	GATCCCTAATGGTGGGG	4423
	CCCCACCAATTAGGGATC	4424
Imidazolinone Resistance ALS	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAACGGTGGGGCTTCAAGGATATGATCCTGG	4425
Zea mays Ser621Asn AGT-AAC	ATGGTGATGGCAGGACTGTGTACTGATCTAA TTAGATCAGTACACAGTCCTGCCATACCATCCAGGATCATATCCT	4426
	TGAAAGCCCCACCGTTAGGGATCATAGGCAACACATGCTCCTGGT	
	GTGGGACGATTATATCCAAGAGGTACGGCC	
	GATCCCTAACGGTGGGG	4427
	CCCCACCGTTAGGGATC	4428
Sulfonylurea Resistance ALS	TCCGCGCTCGCCGACGCCCTCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTCTCGCGCCGCATGATGGCACCGACGCC	4429
Lolium multiflorum Pro167Ser CCG-TCG	TTCCAGGAGACGCCATCGTCGAGGTACCCGCT AGCGGGTGACCTCGACGATGGCGTCTCCTGGAAGGCGTCGGT	4430
	GCCGATCATGCGCGCGAGACCTGCCCGTATGGCCACCATG	
	GGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGCAGGTC <u>T</u> CGCGCCGC	4431
	GCGGCGCG <u>A</u> AGACCTGCC	4432
5 Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Gln CCG-CAG	CCCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCC ATCACGGGGCAGGT <u>C</u> <u>A</u> CGGCCGATGATCGGCACGGACGCT TCCAGGAGACGCCATCGTCGAGGTACCCGCTC	4433
	GAGCGGGTGACCTCGACGATGGCGTCTCTGGAAAGGCGTCCG TGCCGATCATGCGCG <u>T</u> GGACCTGCCCGTGATGGCCACCATG GGGATGGAGTCGAGGGAGGGCGTCGGCGAGCGCGG	4434
	GCAGGT <u>C</u> <u>A</u> CGGCCGCA	4435
	TGCGGCG <u>T</u> GGACCTGC	4436
10 Imidazolinone Resistance ALS <i>Lolium multiflorum</i> Ser623Asn AGC-AAC	CTGGGCCATACTGGATATCATCGTCCCTCACCAAGGAGCATG TGCTGCCTATGATCCCT <u>A</u> <u>CG</u> GTGGTGTTCAGGACATTATCA TGGAAGGTGATGGCAGGATTCGTATTAAC	4437
	GTAAATACGAAATCCTGCCATCACCTCCATGATAATGTCTTG AAGCACCA <u>CG</u> GTAGGGATCATAGGCAGCACATGCTCCTGGTGA GGGACGATGATATCCAACAAGTATGGCCCAG	4438
	GATCCCT <u>A</u> <u>CG</u> GTGGT	4439
	CACCACCG <u>T</u> AGGGATC	4440
15 Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Ser CCA-TCA	TCCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGC CATCACGGCCAGGT <u>C</u> <u>T</u> ACGCCGATGATCGGCACGGACGCGT TCCAGGAGACGCCATAGTGGAGGTACCGC	4441
	AGCGCGTGACCTCCACTATGGCGTCTCTGGAAACGCGTCCGT CCGATCATGCGCG <u>T</u> <u>G</u> AGACCTGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGGAGAGCGTCGGCGAGCGCGGA	4442
	GCCAGGT <u>C</u> <u>T</u> ACGCCGC	4443
	GCGGCGTG <u>A</u> AGACCTGGC	4444
20 Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Gln CCA-CAA	CCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCC ATCACGGCCAGGT <u>C</u> <u>A</u> CGGCCGATGATCGGCACGGACGCGTT CCAGGAGACGCCATAGTGGAGGTACCGC	4445
	GAGCGCGTGACCTCCACTATGGCGTCTCTGGAAACGCGTCCGT CCGATCATGCGCG <u>T</u> <u>G</u> AGACCTGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGGAGAGCGTCGGCGAGCGCGG	4446
	CCAGGT <u>C</u> <u>A</u> CGGCCGCA	4447
	TGCGGCG <u>T</u> GGACCTGG	4448

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
Imidazolinone Resistance ALS <i>Hordeum vulgare</i> Ser524Asn AGC-AAC	CCCAGGGCCGTACCTGCTGGATATCATTGTCGGCATCAGGAGC ACGTGCTGCCTATGATCCAA <u>ACGGTGGT</u> GCTTCAAGGACATGA TCATGGAGGGTGTGGCAGGACCTCGTACTGA	4449
	TCAGTACGAGGTCCCTGCCATCACCCCTCATGATCATGTCCTGAA AGCACCAACCG <u>TTGGG</u> ATCATAGGCAGCACGTGCTCCTGATGCG GGACAATGATATCCAGCAGGTACGGCCCTGGG	4450
	GATCCAA <u>ACGGTGGT</u> G	4451
	CACCACCG <u>TTGGG</u> ATC	4452
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTC <u>CTCGT</u> CGGATGATCGGTACCGATGCTTC CAGGAAACTCCAATTGTTGAGGTAACAAGGT	4453
	ACCTTGTACCTCAACAATTGGAG <u>TTCTGGAA</u> AGCATTGACCGTAC CGATCATCCGACGAG <u>AGACTT</u> GACCAGTGTACGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCAC	4454
	GTCAAGTC <u>CTCGT</u> CGG	4455
	CCGACGAG <u>AGACTT</u> GAC	4456
	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTC <u>ACG</u> TCGGATGATCGGTACCGATGCTTC AGGAAACTCCAATTGTTGAGGTAACAAGGT <u>C</u>	4457
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GACCTTGTACCTCAACAATTGGAG <u>TTCTGGAA</u> AGCATTGACCGTAC CCGATCATCCGACG <u>TTGGACTT</u> GACCAGTGTACGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4458
	TCAAGT <u>CCAACG</u> TCGGA	4459
	TCCGACG <u>TTGGACTT</u> GAC	4460
	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTC <u>CAG</u> CGTCGGATGATCGGTACCGATGCTTC AGGAAACTCCAATTGTTGAGGTAACAAGGT <u>C</u>	4461
	GACCTTGTACCTCAACAATTGGAG <u>TTCTGGAA</u> AGCATTGACCGTAC CCGATCATCCGACG <u>CTGGACTT</u> GACCAGTGTACGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4462
Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	TCAAGT <u>CCACG</u> TCGGA	4463
	TCCGACG <u>CTGGACTT</u> GAC	4464
	GACCTTACTTGTGGATGTGATTGTCACATCAAGAACATGTCCT GCCTATGATCCCC <u>ATGGAGGCG</u> CTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4465
	TGAGGTCAATATTGTGTTCTCCATCACCCCTGTGATCACATCTT TGAAAGCGCCTCC <u>ATTGGGG</u> ATCATAGGCAGGACATGTTCTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4466
	GATCCCC <u>ATGGAGGCG</u>	4467

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCTCCA <u>T</u> GGGGATC	4468
5 Sulfonylurea Resistance ALS <i>Amaranthus</i> <i>retroflexus</i> Pro192Ser CCC-TCC	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTGCC TTACTGGCAAGTT <u>CCCCGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTAACTCGAT	4469
	ATCGAGTTACCTCAACAATTGGAGTCTCTGAAAAGCATCAGTAC AATCATACGCCGG <u>AA</u> ACTGCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4470
	GGCAAGTT <u>CCCCGGCGT</u>	4471
	ACGCCGG <u>AA</u> ACTTGCC	4472
10 Sulfonylurea Resistance ALS <i>Amaranthus</i> <i>retroflexus</i> Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTGCC TTACTGGCAAGTT <u>CAACGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTAACTCGATC	4473
	GATCGAGTTACCTCAACAATTGGAGTCTCTGAAAAGCATCAGTAC CAATCATACGCCG <u>TTGAA</u> CTTGCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4474
	GCAAGTT <u>CAACGGCGT</u> A	4475
	TACGCCG <u>TTGAA</u> CTTG	4476
15 Sulfonylurea Resistance ALS <i>Amaranthus</i> <i>retroflexus</i> Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTGCC TTACTGGCAAGTT <u>CAGCGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTAACTCGATC	4477
	GATCGAGTTACCTCAACAATTGGAGTCTCTGAAAAGCATCAGTAC CAATCATACGCCG <u>CTGAA</u> CTTGCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4478
	GCAAGTT <u>CAGCGCGT</u> A	4479
	TACGCCG <u>CTGAA</u> CTTG	4480
20 Imidazolinone Resistance ALS <i>Amaranthus</i> <i>retroflexus</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCAACATCAGGAGCATGTGC TGCCTATGATCCCT <u>ACCGGTGCCG</u> CTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4481
	ACCAACTAATAAGCCCTTCTTCCATCACCCCTGTGTTATGGTGTCC TGAAGGCGGCACCG <u>TTAGGG</u> ATCATAGGCAGCAGCATGCTCCTGA TGTGGTACGATTACATCCAGCAGATA <u>CGGTC</u>	4482
	GATCCCT <u>ACCGGTGCCG</u>	4483
	CGGCACCG <u>TTAGGG</u> ATC	4484

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:	
5 Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Ser CCA-TCA	AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGTGT <u>CACGTAGGATGATAGGTACTGATGCTTT</u> CAGGAAACTCCTATTGTTGAGGTAACTAGAT	4485	
	ATCTAGTTACCTCAACAATAGGAGTTCTGAAAAGCATCAGTACC TATCATCCTACGT <u>GACACTTGACCTGTTAGCAACAATGGGGAC</u> GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4486	
	<u>GTCAAGTGT</u> <u>CACGTAGG</u>	4487	
	CCTACGT <u>GACACTTGAC</u>	4488	
10 Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Gln CCA-CAA	GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGT <u>GCAACGTAGGATGATAGGTACTGATGCTTT</u> CAGGAAACTCCTATTGTTGAGGTAACTAGATC	4489	
	GATCTAGTTACCTCAACAATAGGAGTTCTGAAAAGCATCAGTAC CTATCATCCTACGT <u>TGCACTTGACCTGTTAGCAACAATGGGGAC</u> CGCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4490	
	<u>TCAAGTGC</u> <u>AACGTAGGA</u>	4491	
	TCCTACGT <u>TGCACTTGA</u>	4492	
	15 Imidazolinone Resistance ALS 1 <i>Nicotiana tabacum</i> Ser650Asn AGT-AAT	GCCATACTTGGATGTATTGTACCTCATCAGGAACATGTTT ACCTATGATT <u>CCCAATGGCGGAGCTTCAAAGATGTGATCACAGA</u> GGGTGACGGGAGAAGTTCTATTGAGTTG	4493
	CAAACTCATAGGAACCTCTCCGTACCCCTGTGATCACATCTT TGAAAGCTCCGCCATTGGGAATCATAGGTAAAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4494	
	<u>GATTCCCAATGGCGGAG</u>	4495	
	CTCCGCCATTGGGAATC	4496	
	20 Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACC <u>GGTCAAGTGT</u> <u>CACGTAGGATGATCGGTACTGATGCTTT</u> CAGGAAACTCCGATTGTTGAGGTAACTAGAT	4497
	ATCTAGTTACCTCAACAATCGGAGTTCTGAAAAGCATCAGTACC GATCATCCTACGT <u>GACACTTGACCCGGTTAGCAACAATGGGGAC</u> GCTATCCAGTAGGGCGTCCCGAGGCCACT	4498	
	<u>GTCAAGTGT</u> <u>CACGTAGG</u>	4499	
	CCTACGT <u>GACACTTGAC</u>	4500	
	25 Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACC <u>GGTCAAGTGC</u> <u>AACGTAGGATGATCGGTACTGATGCTTT</u> CAGGAAACTCCGATTGTTGAGGTAACTAGATC	4501
	GATCTAGTTACCTCAACAATCGGAGTTCTGAAAAGCATCAGTAC CGATCATCCTACGT <u>TGCACTTGACCCGGTTAGCAACAATGGGGAC</u> CGCTATCCAGTAGGGCGTCCCGAGGCCAC	4502	
	<u>TCAAGTGC</u> <u>AACGTAGGA</u>	4503	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCCTACGT <u>T</u> GCACTTGA	4504
5 Imidazolinone Resistance ALS 2 <i>Nicotiana tabacum</i> Ser647Asn AGT-AAT	GGCCATACTTGTGGATGTGATTGTACCTCATCAGGAACATGTCT ACCTATGATT <u>CCCA</u> <u>A</u> TGGCGGGGCTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAAGTTCCATTGACTTG	4505
	CAAAGTCAATAGGAAC <u>T</u> CTCCCGTCACCCCTGTGATCACATCTT TGAAAGCCCCGCC <u>A</u> TTGGGAATCATAGGTAGAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4506
	GATT <u>CCCA</u> <u>A</u> TGGCGGGG	4507
	CCCCGCC <u>A</u> TTGGGAATC	4508
	AGTGGCTTGTGATGCTTATTAGACAGTGTCCAATGGTTGCTA TTACTGGTCAAG <u>T</u> <u>T</u> CCAGGAGAA <u>T</u> ATTGGAACAGATGCGTTCA AGAAACCC <u>C</u> <u>T</u> ATTGTTGAGGTAACACGTT	4509
10 Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Ser CCC-TCC	AACGTGTTACCTCAACAATAGGGGTTCTGAAACGCATCTGTTCC AATCATTCTCCTGG <u>A</u> ACTTGACCAGTAATAGCAACCATTGGAAC CTGTCTAATAAAAGCATCAGCAAGACCAC	4510
	GTCAAG <u>T</u> <u>T</u> CCAGGAGA	4511
	TCTCCTGG <u>A</u> ACTTGAC	4512
	GTGGCTTGTGATGCTTATTAGACAGTGTCCAATGGTTGCTAT TACTGGTCAAG <u>T</u> <u>C</u> <u>A</u> AGGAGAA <u>T</u> ATTGGAACAGATGCGTTCA AGAAACCC <u>C</u> <u>T</u> ATTGTTGAGGTAACACGTT	4513
	GAACGTGTTACCTCAACAATAGGGGTTCTGAAACGCATCTGTTCC CAATCATTCTCCT <u>T</u> GA <u>A</u> CTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAAGCATCAGCAAGACCAC	4514
15 Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAA	TCAAG <u>T</u> <u>C</u> <u>A</u> AGGAGAA	4515
	TTCTCCT <u>T</u> GA <u>A</u> CTTG	4516
	GTGGCTTGTGATGCTTATTAGACAGTGTCCAATGGTTGCTAT TACTGGTCAAG <u>T</u> <u>C</u> <u>A</u> AGGAGAA <u>T</u> ATTGGAACAGATGCGTTCA AGAAACCC <u>C</u> <u>T</u> ATTGTTGAGGTAACACGTT	4517
	GAACGTGTTACCTCAACAATAGGGGTTCTGAAACGCATCTGTTCC CAATCATTCTCCT <u>T</u> GA <u>A</u> CTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAAGCATCAGCAAGACCAC	4518
	TCAAG <u>T</u> <u>C</u> <u>A</u> AGGAGAA	4519
20 Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAG	TTCTCCT <u>T</u> GA <u>A</u> CTTG	4520
	GGGCCTTACTTGTGGATGTGATCGTGCCCCATCAAGAACATGTG TTGCCCATGAT <u>CCCG</u> <u>A</u> ATGGTGGAGGTTCATGGATGTGATCACCC GAAGGGCGACGGCAGAA <u>T</u> ATTGAGCTT	4521
	AAGCTCAATATTCA <u>T</u> CGCCGTGCCTCGGTGATCACATCCAT GAAACCTCCACC <u>A</u> TT <u>C</u> GGGATCATGGGCAACACATGTTCTGATG GGGCACGATCACATCCAACAAGTAAGGCC	4522
25 Imidazolinone Resistance ALS <i>Xanthium</i> spp. Ala631Asn GCT-AAT		
30 GCT-AAT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TGATCCC <u>GAATGGT</u> GA	4523
	TCCACC <u>ATCGGG</u> ATCA	4524
5 Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Ser CCG-TCG	TCCGGGTTGCTGATGCTTGCTCGATTCCGTTCCACTGGTGGCG ATCACGGGGCAGGTG <u>T</u> CGCGGCGAATGATTGGGACGGATGCTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT	4525
	ACCGTGTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CAATCATTGCCCG <u>G</u> ACACCTGCCCGTGATGCCACCAGTGG ACGGAATCGAGCAAAGCATCAGCAAACCCGGA	4526
	GGCAGGTG <u>T</u> CGCGGCGA	4527
	TCGCCGCC <u>G</u> ACACCTGCC	4528
	CCGGGTTGCTGATGCTTGCTCGATTCCGTTCCACTGGTGGCGA TCACGGGGCAGGTG <u>C</u> AGCGGCGAATGATTGGGACGGATGCTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC	4529
10 Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Gln CCG-CAG	GACCGTGTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CCAATCATTGCCG <u>T</u> GCACCTGCCCGTGATGCCACCAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCG GCAGGTG <u>C</u> AGCGGCGAA	4530
	TTGCCG <u>G</u> TCACCTGC	4531
		4532
	GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC TGCCTATGATTCT <u>A</u> TGGTGCAGCCTCAAGGATATCATTAAACGA AGGTGATGGAAGAACAAAGTTATTGATGTT	4533
	GAACATCAATAACTTGTCTTCCATCACCTCGTTAATGATATCCTT GAAGGCTGCACC <u>A</u> TTAGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	4534
15 Imidazolinone Resistance ALS <i>Bassia scoparia</i> Ser649Asn AGT-AAT	GATTCT <u>A</u> ATGGTGCAG	4535
	CTGCACCA <u>A</u> TTAGGAATC	4536
20 Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Ser CCT-TCT	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTCCCTTGTCGC CATTACAGGACAGGT <u>C</u> CTCGCCGGATGATCGGTACTGACGCCCT CCAAGAGACACCAATCGTTGAGGTAACGAGGT	4537
	ACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTAC CGATCATCCGGCGAG <u>A</u> GCACCTGTCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4538
	GACAGGT <u>C</u> CTCGCCGG	4539
	CCGGCGAG <u>A</u> GCACCTGTC	4540

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAA	GCGGGTTAGCAGACGCGATGCTTGACAGTGTCCCTTGTGCC ATTACAGGACAGGT <u>CCAAC</u> CGCCGGATGATCGGTACTGACGCC CCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4541
	GACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTA CCGATCATCCGGCG <u>TTGG</u> ACCTGTCCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	4542
	ACAGGT <u>CCAAC</u> GCCGGA	4543
	TCCGGCG <u>TTGG</u> ACCTGT	4544
	GCGGGTTAGCAGACGCGATGCTTGACAGTGTCCCTTGTGCC ATTACAGGACAGGT <u>CCAAG</u> CGCCGGATGATCGGTACTGACGCC CCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4545
10 Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAG	GACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTA CCGATCATCCGGCG <u>CTGG</u> ACCTGTCCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	4546
	ACAGGT <u>CCAAG</u> GCCGGA	4547
	TCCGGCG <u>CTGG</u> ACCTGT	4548
	GACCATACTGTTGGATGTGATATGTCGCACCAAGAACATGTGT TACCGATGAT <u>CCCCAA</u> ATGGTGGCACTTCAAAGATGTAATAACAGA AGGGGATGGTCGCACTAAGTACTGAGAGAT	4549
	ATCTCTCAGTACTTAGTGCACCACCCCTCTGTTATTACATCTT TGAAAGTGCCACCA <u>TTGG</u> GATCATCGGTACACATGTTCTTGGT GCGGACATATCACATCCAACAGGTATGGTC	4550
15 Imidazolinone Resistance ALS 1 <i>Brassica napus</i> Ser638Asn AGT-AAT	GAT <u>CCCCAA</u> ATGGTGGCA	4551
	TGCCACCA <u>TTGG</u> GATC	4552
	CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTCCCTTGTCG CCATTACAGGACAGGT <u>CCCTCGCCGG</u> ATGATCGGTACTGACGCC TTCCAAGAGACACCAATCGTTGAGGTAACGAGG	4553
	CCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTAC GATCATCCGGCGAGGA <u>ACCTGTCC</u> CTGTAATGGCGACAAGAGGAA CACTGTCAAGCATCGCGTCTGCTAACCCGCTG	4554
	GGACAGGT <u>CCCTCGCCG</u>	4555
20 Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Ser CCC-TCC	CGGGCGAGGA <u>ACCTGTCC</u>	4556
	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTCCCTTGTGC CATTACAGGACAGGT <u>CACTCGCCGG</u> ATGATCGGTACTGACGCC TCCAAGAGACACCAATCGTTGAGGTAACGAGGT	4557
	ACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCGTCAGTAC CGATCATCCGGCGAG <u>TGACCTGTCC</u> CTGTAATGGCGACAAGAGGAA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4558
	GACAGGT <u>CACTCGCCG</u>	4559

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGGCGAG <u>T</u> GACCTGTC	4560
5 Imidazolinone Resistance ALS 2 <i>Brassica napus</i> Ser582Asn AGT-AAT	GACCATACTGTTGGATGTGATATGTCGCACCAAGAACATGTGT TACCGATGAT <u>CCCAA</u> <u>A</u> TGGTGGCACTTCAAAGATGTAATAACAGA AGGGGATGGTCGCACTAAGTACTGAGAGAT	4561
	ATCTCTCAGTACTTAGTGC <u>G</u> ACC <u>AT</u> CCCCTCTGTTATTACATCTT TGAAAGTGC <u>C</u> ACC <u>AT</u> GGGATCATCGGTAACACATGTTCTGGT GCGGACATATCACATCCAACAGGTATGGTC	4562
	GAT <u>CCCAA</u> <u>A</u> TGGTGGCA	4563
	TGCCACC <u>AT</u> GGGATC	4564
10 Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGCGATGCTTGACAGTGTCCCTCTCGTCGC CATCACAGGACAGGT <u>C</u> TC <u>T</u> CGCCGGATGATCGGTACTGACGCGT TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT	4565
	ACCTCGTTACCTCAACGATTGGCGTCTTGGAACCGCGTCAGTAC CGATCATCCGGCGAG <u>A</u> GACCTGTCC <u>T</u> GTGATGGCGACGAGAGGA ACACTGTCAAGCATCGCGTCGGCTAACCGCT	4566
	GACAGGT <u>C</u> TC <u>T</u> CGCCGG	4567
	CCGGCGAG <u>A</u> GACCTGTC	4568
15 Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAA	GC <u>GGGTTAGCCGACGCGATGCTTGACAGTGTCCCTCTCGTCGCC</u> ATCACAGGACAGGT <u>CC</u> <u>A</u> CGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGT	4569
	GACCTCGTTACCTCAACGATTGGCGTCTTGGAACCGCGTCAGTA CCGATCATCCGGCG <u>T</u> GGACCTGTCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCGC	4570
	ACAGGT <u>CC</u> <u>A</u> CGCCGG	4571
	TCCGGCG <u>T</u> GGACCTGT	4572
20 Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAG	GC <u>GGGTTAGCCGACGCGATGCTTGACAGTGTCCCTCTCGTCGCC</u> ATCACAGGACAGGT <u>CC</u> <u>A</u> CGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGT	4573
	GACCTCGTTACCTCAACGATTGGCGTCTTGGAACCGCGTCAGTA CCGATCATCCGGCG <u>T</u> GGACCTGTCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCGC	4574
	ACAGGT <u>CC</u> <u>A</u> CGCCGG	4575
	TCCGGCG <u>T</u> GGACCTGT	4576
25 Imidazolinone Resistance ALS 3 <i>Brassica napus</i> Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGT <u>C</u> ATCTGTC <u>CC</u> GCACCAAGAACATGTGT TACCGATGAT <u>CCCAA</u> <u>A</u> TGGTGGCACTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4577
	ATCTCTCAGTACTTAGTGC <u>G</u> ACC <u>AT</u> CCCCTCTGGTTATTACATCTT TGAAAGTGC <u>C</u> ACC <u>AT</u> GGGATCATCGGTAACACATGTTCTGGT GCGGACAGATGACATCCAACAGGTACGGTC	4578

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCCCAA <u>A</u> GGTGGCA	4579
	TGCCACCA <u>TT</u> GGGATC	4580
5 Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGATGGTCG CCATCACGGGCCAGGT <u>C</u> CCGCCATGATCGGACCGACGC CTTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4581
	AGCGGGTGACCTCGACTATGGCGTCTCCTGGAAGGCGTCGGT CCGATCATGCGGCCGG <u>A</u> GACCTGGCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGGA	4582
	GCCAGGT <u>C</u> CCGCCGC	4583
	GC <u>GGCGGGAGACCTGGC</u>	4584
	CCGCGCTCGCCGACGCGCTGCTCGACTCCGATGGTCG CATCACGGGCCAGGT <u>CC</u> ACGCCATGATCGGACCGACGCC TTCCAGGAGACGCCATAGTCGAGGTACCCGCTC	4585
10 Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	GAGCGGGTGACCTCGACTATGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGCG <u>T</u> GGACCTGGCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4586
	CCAGGT <u>CC</u> ACGCCGCA	4587
	TGCGGCG <u>T</u> GGACCTGG	4588
	CCGCGCTCGCCGACGCGCTGCTCGACTCCGATGGTCG CATCACGGGCCAGGT <u>CC</u> AGCGCCATGATCGGACCGACGCC TTCCAGGAGACGCCATAGTCGAGGTACCCGCTC	4589
	GAGCGGGTGACCTCGACTATGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGCG <u>T</u> GGACCTGGCCGTGATGGCGACCATCG GGGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4590
15 Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	CCAGGT <u>CC</u> AGCGCCGCA	4591
	TGCGGCG <u>T</u> GGACCTGG	4592
	GGCCATA <u>CTTGGATATCGTCCC</u> GACCGAGGACATGTGC TGCCTATGAT <u>CCCAA</u> ATGGGGCGCATCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4593
	ATAGATTAATACACAGTCCTGCCATACCATCCAGGATCATGTCTCT TGAATGCGCCCC <u>AT</u> GGGATCATAGGCAGCACATGCTCTGGT GCGGGACGATGATCCAACAAGTATGGCC	4594
	GATCCCAA <u>A</u> GGGGCG	4595
20 Imidazolinone Resistance ALS <i>Oryza sativa</i> Ser627Asn AGT-AAT	CGCCCC <u>CA</u> TTGGGATC	4596

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	TCTGCGCTCGCAGACGCGTTGCTCGACTCCGCCCCATGGTCGC CATCACGGGACAGGTG <u>T</u> CGCGACGCATGATTGGCACCGACGCC TTCAGGAGACGCCATCGTCGAGGTCAACCGCT	4597
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGT CCAATCATGCGTCGC <u>G</u> ACACCTGTCCGTGATGGCGACCATGG GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	4598
	GACAGGTG <u>T</u> CGCGACGC	4599
	GCGTCGCG <u>A</u> CACCTGT	4600
10 Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CTGCGCTCGCAGACGCGTTGCTCGACTCCGCCCCATGGTCGCC ATCACGGGACAGGTG <u>C</u> AGCGACGCATGATTGGCACCGACGCC TCAGGAGACGCCATCGTCGAGGTCAACCGCTC	4601
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGT GCCAATCATGCGTCG <u>C</u> GCACCTGTCCGTGATGGCGACCATGG GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	4602
	ACAGGTG <u>C</u> AGCGACGC	4603
	TGCCTCGC <u>T</u> GCACCTGT	4604
	GGCCGTACCTCTGGATATAATCGTCCCGACCAGGAGCATGTGT TGCCTATGATCCCT <u>A</u> ATGGTGGGGCTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTATTGATCCGT ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCC TTGAAAGCCCCACCA <u>T</u> AGGGATCATAGGCAACACATGCTCCTGG TGCGGGACGATTATATCCAAGAGGTACGGCC GATCCCT <u>A</u> ATGGTGGGG CCCCACCA <u>T</u> AGGGATC	4605 4606 4607 4608
20 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGT <u>C</u> TCGTCGGATGATCGGTACCGATGCTTC CAGGAAACTCCAATTGTTGAGGTAAAGGT	4609
	ACCTTGTACCTCAACAATTGGAGTTCCCTGGAAAGCATCGGTAC CGATCATCCGACGAG <u>A</u> GACTTGACCAAGTGTACGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4610
	GTCAAGTCT <u>C</u> CGTCGG	4611
	CCGACGAGAG <u>A</u> TTGAC	4612
	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGT <u>C</u> ACGTCGGATGATCGGTACCGATGCTTC AGGAAACTCCAATTGTTGAGGTAAAGGT GACCTTGTACCTCAACAATTGGAGTTCCCTGGAAAGCATCGGTAC CCGATCATCCGACG <u>T</u> GGACTTGACCAAGTGTACGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCACT TCAAGT <u>C</u> CAACGTCGGA	4613 4614 4615

Phenotype: Gene Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCCGACGT <u>GG</u> ACTTGA	4616
5 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGT <u>CCAGCG</u> CGGATGATCGGTACCGATGCTTCC AGGAAACTCCAATTGTTGAGGTAAACAGGTC	4617
	GACCTTGTACCTCAACAATTGGAGTTCCCTGGAAAGCATCGGT CCGATCATCCGAC <u>GG</u> ACTTGACCAAGTGTACGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4618
	TCAAGT <u>CCAGCG</u> TCGGA	4619
	TCCGACG <u>CTGG</u> ACTTGA	4620
	GACCTTACTTGTGGATGTATTGTCCCACATCAAGAACATGTCC GCCTATGATCCCC <u>ATGGAGGG</u> CTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTA	4621
10 Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	TGAGGTCAATATTGTGTTCTCCATCACCCCTGTGATCACATCTT TGAAAGCCCCTCC <u>ATTGGGG</u> ATCATAGGCAGGACATGTTCTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4622
	GATCCCC <u>ATGGAGGG</u>	4623
	CCCCTCC <u>ATTGGGG</u> ATC	4624
	TCTGGTCTTGCTGATGCAC <u>TTGACTCAG</u> CCCTCTGCGCC ATTACTGGGCAAGT <u>TTCCCCGG</u> GTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGAT	4625
	ATCGAGTTACCTCAACAATTGGAGTCTCTGAAAAGCATCAGTACC AATCATACGCCGG <u>AAACTG</u> CCCAGTAATGGCGACAAGAGGG CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4626
15 Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Ser CCC-TCC	GGCAAGT <u>TTCCCCGG</u> GT ACGCCGG <u>AAACTG</u> CC	4627 4628
	CTGGTCTTGCTGATGCAC <u>TTGACTCAG</u> CCCTCTGCGCC TTACTGGGCAAGT <u>TCACGG</u> CGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4629
	GATCGAGTTACCTCAACAATTGGAGTCTCTGAAAAGCATCAGTAC CAATCATACGCCG <u>TTGA</u> ACTGCCAGTAATGGCGACAAGAGGG CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4630
	GCAAGT <u>TCACGG</u> GT TACGCCG <u>TTGA</u> ACTTGC	4631 4632
	CTGGTCTTGCTGATGCAC <u>TTGACTCAG</u> CCCTCTGCGCC TTACTGGGCAAGT <u>TCAGCG</u> CGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4633
20 Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAA	GATCGAGTTACCTCAACAATTGGAGTCTCTGAAAAGCATCAGTAC CAATCATACGCCG <u>CTGA</u> ACTGCCAGTAATGGCGACAAGAGGG CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4630
	GCAAGT <u>TCACGG</u> GT TACGCCG <u>TTGA</u> ACTTGC	4631 4632
25 Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCAC <u>TTGACTCAG</u> CCCTCTGCGCC TTACTGGGCAAGT <u>TCAGCG</u> CGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4633
	GATCGAGTTACCTCAACAATTGGAGTCTCTGAAAAGCATCAGTAC CAATCATACGCCG <u>CTGA</u> ACTGCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4634

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Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCAAGTT <u>CAGCGGCGTA</u>	4635
	TACGCC <u>GCTGAAC</u> TTGC	4636
Imidazolinone Resistance ALS <i>Amaranthus powellii</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCA <u>CACATCAGGAGCATGTGC</u> TGCCTATGATCC <u>CTAACGGTGC</u> CGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4637
	ACCAACTAATAAGCC <u>TTCTTCCATCAC</u> CCCTCTGTTATGGTGCCT TGAAGGCGGCACCG <u>GTAGGGATCATAGG</u> CAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATA <u>CGGTC</u>	4638
	GATCC <u>CTAACGGTGCCG</u>	4639
	CGGCACCG <u>GTAGGGATC</u>	4640

**Table 12**  
**Genome-Altering Oligos Conferring Porphyric Herbicide Resistance**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Porphyric Herbicide Resistant PPO <i>Arabidopsis thaliana</i> Val365Met GTT-ATG	TCTTGC <del>GGCC</del> CTTCTGAATCTGCTGCAAATGCACTCTCAAAACT ATATTACCCACCA <del>ATGG</del> CAGCAGTATCTATCTGTACCCGAAAGA AGCAATCCGAACAGAATGTTGATAGATGG	4641
		CCATCTATCAAACATTCTGTCGGATTGCTTCTTCGGGTACGAGA TAGATACTGCTG <del>CC</del> <del>ATGG</del> TGGTGGTAATATAGTTTGAGAGTGCATT TGCAGCAGATTAGAAAGAGGGCGCAAGA	4642
		CCCACCA <del>ATGG</del> CAGCAG	4643
		CTGCTGCC <del>CA</del> <del>ATGG</del> GGGG	4644
10	Porphyric Herbicide Resistant PPO <i>Nicotiana tabacum</i> Val376Met GTT-ATG	TATTACGTCCCTTTCGGTTGCCGCAGCAGATGCAC <del>TT</del> CAAATT CTACTATCCCCA <del>ATGG</del> GAGCAGTCACAATTTCATATCCTCAAGAA GCTATTCTGTGATGAGCGTCTGGTTGATGG	4645
		CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAA ATTGTGACTGCTCC <del>CA</del> <del>ATGG</del> GGGGATAGTAGAAATTGAAAGTGCA TCTGCTGCCAACC <del>GA</del> AGAGGACGTAATA	4646
		TCCCCCA <del>ATGG</del> GAGCAG	4647
		CTGCTCCC <del>CA</del> <del>ATGG</del> GGGG	4648
		TGTTGCGTCCGCTTCTGTTGGGTGCAGCAGATGCATTGTCAAAT TTTATTATCCTCCG <del>ATGG</del> CAGCTGTATCAATTTCATATCCAAAAGA CGCAATTCTGTGCTGACCGGCTGATTGATGG	4649
15	Porphyric Herbicide Resistant PPO <i>Cichorium intybus</i> Val383Met GTT-ATG	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTGGATATGAA ATTGATACAGCTGCC <del>CA</del> <del>TC</del> GGAGGATAATAAAATTGACAATGCAT CTGCTGCCACCCAA <del>CG</del> AAAGCGGGACGCAACA	4650
		TCCTCCG <del>ATGG</del> CAGCTG	4651
		CAGCTGCC <del>CA</del> <del>TC</del> GGAGGA	4652
		TCCTTCGTC <del>CC</del> ACTTCAGATGTCGCCAGAATCTCTTCAAATT TCATTATCCACCA <del>ATGG</del> CAGCTGTGTCACTTCTATCCTAAAGAA GCAATTAGATCAGAGTGCTTGATTGACGG	4653
		CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTAGGATAGGAAA GTGACACAGCTGCC <del>CA</del> <del>ATGG</del> GGATAATGAAATTGAAAGAGATTG TGC <del>GG</del> GCACATCTGAAAGTGGACGAAGGA	4654
20	Porphyric Herbicide Resistant PPO <i>Spinacia oleracea</i> Val390Met GTT-ATG	TCCACCA <del>ATGG</del> CAGCTG	4655
		CAGCTGCC <del>CA</del> <del>ATGG</del> GGGA	4656

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Porphyric Herbicide Resistant PPO <i>Zea mays</i> Val363Met GTT-ATG	TTTGCCTTCACTTCAAGCGATGCTGCAGATGCTCTATCAAGATTCTATTATCCACCG <u>A</u> T <u>GG</u> GCTGCTGTAACGTGTTCGTATCCAAAGGAA GCAATTAGAAAAGAATGCTTAATTGATGG	4657
	CCATCAATTAAAGCATTCTTCTAATTGCTTCTTGGATACGAAACAGTTACAGCAG <u>C</u> <u>A</u> T <u>CG</u> GTGGATAATAGAATCTTGATAGAGCATCTGCAGCATCGCTGAAAGTGGACGCAAAA	4658
	TCCACCG <u>A</u> T <u>GG</u> GCTGCTG	4659
	CAGCAG <u>C</u> <u>A</u> T <u>CG</u> GTGG	4660
10 Porphyric Herbicide Resistant PPO <i>Oryza sativa</i> Val364Met GTT-ATG	TCTTGCGCCACTTCAAGTGATGCAGCAGATGCTCTGTCAATATTCTATTATCCACCA <u>A</u> T <u>GG</u> GCTGCTGTAACGTGTTCATATCCAAAGAA GCAATTAGAAAAGAATGCTTAATTGACGG	4661
	CCGTCAATTAAAGCATTCTTCTAATTGCTTCTTGGATATGAAACAGTTACAGCAG <u>C</u> <u>A</u> T <u>GG</u> GTGGATAATAGAATATTGACAGAGCCTCTGCTGCATCACTGAAAGTGGCCGCAAGA	4662
	TCCACCA <u>A</u> T <u>GG</u> GCTGCTG	4663
	CAGCAG <u>C</u> <u>A</u> T <u>GG</u> GTGG	4664
15 Porphyric Herbicide Resistant PPO <i>Chlamydomonas reinhardtii</i> Val389Met GTG-ATG	CTGGTCAAGGAGCAGGCGCCGCCGCCGCCGCCGAGGCCCTGGGCTCCTCGACTACCCGCC <u>A</u> T <u>GG</u> GCGCCGTGACGCTGTCGTACCCG CTGAGCGCCGTGCGGGAGGGAGCGCAAGGCCCTCGG	4665
	CCGAGGCCTTGCCTCCCTCCGCACGGCGCTCAGCGGGTACGA CAGCGTCACGGGCC <u>A</u> T <u>CG</u> CGGGTAGTCGAAGGGAGCCCAGG GCCTCGGGCGGGCGGGCGCCTGCTCCTGACCAG	4666
	ACCCGCC <u>A</u> T <u>GG</u> GC	4667
	GGCGCC <u>C</u> <u>A</u> T <u>CG</u> CGGGT	4668

20

Table 13  
Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
25 Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGATTCCAATATGCT <u>A</u> TTCAACAATTCTCGTTCTTACATTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	4669
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGAAAGAA CGAGAATTGTTGAA <u>A</u> GTAGCATATTGAAAATCAATCGGCCAAAT AACCGTGAGCAGCTACAATGTTGTAAGTT	4670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATATGCT <u>ACT</u> TTCAACA	4671
	TGTTGAA <u>AG</u> TAGCATAT	4672
5 Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACACTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAA <u>AG</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTATAAGTT	4673
	ATATGCT <u>ACT</u> TTCAACA	4674
	TGTTGAA <u>AG</u> TAGCATAT	4675
	ATATGCT <u>ACT</u> TTCAACA	4676
10 Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACACTCGTCTTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAA <u>AG</u> TAGCATATTGGAAGATCAATCGGCCAAAA AACCATGAGCGGCTACGATATTATAAGTT	4677
	ATATGCT <u>ACT</u> TTCAACA	4678
	TGTTAAA <u>AG</u> TAGCATAT	4679
	ATATGCT <u>ACT</u> TTCAACA	4680
15 Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACACTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAA <u>AG</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTT	4681
	ATATGCT <u>ACT</u> TTCAACA	4682
	TGTTGAA <u>AG</u> TAGCATAT	4683
	ATATGCT <u>ACT</u> TTCAACA	4684
20 Triazine Resistant D1 Protein <i>Magnolia pyramidalis</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACACTCGTTCGTTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGAATGTAAAGAA CGAGAATTGTTGAA <u>AG</u> TAGCATATTGGAAGATCAATCGGCCAAAA AACCATGAGCAGCTACGATATTATAAGTT	4685
	ATATGCT <u>ACT</u> TTCAACA	4686
	TGTTGAA <u>AG</u> TAGCATAT	4687
	ATATGCT <u>ACT</u> TTCAACA	4688
25 Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT	AAACCTATAATATTGAGCAGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACACTCGTTCGTTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGAATGTAAAGAA CGAGAGTTGTTGAA <u>AG</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAAGTT	4689
	ATATGCT <u>ACT</u> TTCAACA	4690

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	TGTTGAAAGTAGCATAT	4692
	AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTTCAACAATTCTCGTTCTTACATTCTCT	4693
	TAGCTGCTTGGCCTGTAGTAGGTATTTG CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT	4694
	AACCATGAGCAGCTACAATATTAGGTTT ATATGCAACTTTCAACA	4695
	TGTTGAAAGTAGCATAT	4696
10 Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTACATTCTCT	4697
	TAGCGGCTTGGCCGGTAGTAGGTATTTG CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT	4698
	AACCGTGAGCAGCTACAATGTTGAAGTTT ATATGCTACTTTCAACA	4699
	TGTTGAAAGTAGCATAT	4700
	AAACTTATAATATTGTGGCCGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTACTTTAACAACTCTCGTTCTTACACTCTCT	4701
15 Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	TGGCTGCTTGGCCTGTAGTAGGGATTG CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT	4702
	AACCATGAGCGGCCACAATATTATAAGTTT ATATGCTACTTTAACAA	4703
	TGTTAAAAGTAGCATAT	4704
	AGACTTATAATATTGTGGCTGCTCACGGTTATTTGGTCGATTAAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTACACTCTCT	4705
	TGGCTGCTTGGCCTGTAGTAGGGATCTG CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCCAAAAT	4706
20 Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	AACCGTGAGCAGCCACAATATTATAAGTCT ATATGCTACTTTAACAA	4707
	TGTTGAAAGTAGCATAT	4708
	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT TTTCCAATATGCTACTTTCAACAATTCTCGTTCTTACATTCTCT	4709
	AGCGGCTTGGCCGGTAGTAGGTATTTG CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCCAAAAT	4710
	AACCGTGAGCAGCTACAATGTTGAAGTTT ATATGCTACTTTAACAA	4711
25 Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	TGTTGAAAGTAGCATAT	4712

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACA <u>ACT</u> CTCGTT <u>CGT</u> AC <u>ACT</u> TTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4713
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAA <u>CGAA</u> CGAGAGTTGTTGAA <u>AGT</u> AGCATATTGGAAGATCAATCGGCCAAA TAACC <u>AT</u> GAGCGGCTACGATGTATAAGTTT	4714
	ATATGCT <u>ACT</u> TTCAACA	4715
	TGTTGAA <u>AGT</u> AGCATAT	4716
10 Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACA <u>ACT</u> CTCGCT <u>CTT</u> AC <u>ACT</u> TTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4717
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAA <u>ATGTAAAGAG</u> CGAGAGTTGTTAAA <u>AGT</u> AGCATATTGGAAGATCAATCGGCCAAA AACC <u>AT</u> GAGCGGCTACGATATTATAAGTTT	4718
	ATATGCT <u>ACT</u> TTCAACA	4719
	TGTTAAA <u>AGT</u> AGCATAT	4720
15 Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACA <u>ACT</u> CTCG <u>CTT</u> AC <u>ACT</u> TTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4721
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAA <u>CGAA</u> CGAGAGTTGTTGAA <u>AGT</u> AGCATATTGGAAGATCAATCGGCCAAA TAACC <u>AT</u> GAGCGGCTACGATATTATAAGTTT	4722
	ATATGCT <u>ACT</u> TTCAACA	4723
	TGTTGAA <u>AGT</u> AGCATAT	4724
20 Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACA <u>ATT</u> CTCG <u>CTT</u> AC <u>ATT</u> CTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4725
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAG <u>ATGTAAAGAA</u> CGAGAATTGTTGAA <u>AGT</u> AGCATATTGGAAGATCAATCGGCCAAA AACC <u>AT</u> GAGCAGCTACGATATTATAAGTTT	4726
	ATATGCT <u>ACT</u> TTCAACA	4727
	TGTTGAA <u>AGT</u> AGCATAT	4728
25 Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT	AAACCTATAATATTGAGCAGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACA <u>ACT</u> CTCG <u>CTT</u> AC <u>ATT</u> CTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4729
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAG <u>ATGTAAAGAA</u> CGAGAGTTGTTGAA <u>AGT</u> AGCATATTGGAAGATCAATCGGCCAAA TAACC <u>AT</u> GAGCTGCTAC <u>AA</u> ATTATAAGTTT	4730
	ATATGCT <u>ACT</u> TTCAACA	4731
	TGTTGAA <u>AGT</u> AGCATAT	4732

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTCAACAATTCTGTTCTTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTG	4733
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCAGCAGCTACAATATTAGGTTT	4734
	ATATGCAACTTCAACA	4735
	TGTTGAAAGTAGCATAT	4736
10 Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAATTCTGTTCTTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTG	4737
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCCTGAGCAGCTACAATGTTGTAAGTTT	4738
	ATATGCTACTTCAACA	4739
	TGTTGAAAGTAGCATAT	4740
15 Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTACTTTAACAACTCTGTTCTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTG	4741
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCAGCAGCCACAATATTATAAGTTT	4742
	ATATGCTACTTTAACAA	4743
	TGTTAAAAGTAGCATAT	4744
20 Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTGGTCGATTAAT CTTCCAATATGCTACTTCAACAATTCTGTTCTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4745
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCCAAAAT AACCCTGAGCAGCCACAATATTATAAGTCT	4746
	ATATGCTACTTCAACA	4747
	TGTTGAAAGTAGCATAT	4748
25 Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT TTTCCAATATGCTACTTCAACAATTCTGTTCTTACATTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTG	4749
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCCAAAAT AACCCTGAGCAGCTACAATGTTGTAAGTTT	4750
	ATATGCTACTTCAACA	4751
	TGTTGAAAGTAGCATAT	4752

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Triazine Resistant D1 Protein <i>Picea abies</i> Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTCGGCCGATTGAT CTTCCAGTATGCT <u>ACT</u> TTCAACAACCTCCCGTTCTTACATTCTTCT TAGCTGCTTGGCCCGTAGCAGGTATCTG	4753
		CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGGGAGTTGTTGAAAGTAGCATACTGGAAGATCAATCGGCCAAA TAACCGTGAGCAGGCCACAATATTGTAGGTTT	4754
		GTATGCT <u>ACT</u> TTCAACA	4755
		TGTTGAAAGTAGCATA	4756
10	Triazine Resistant D1 Protein <i>Vicia faba</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAATTCTCGCTCTTACATTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4757
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATATTATAGGTTT	4758
		ATATGCT <u>ACT</u> TTCAACA	4759
		TGTTGAAAGTAGCATAT	4760
		AGACTTATAATATTGTGGCTGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCT <u>ACT</u> TTCAACAACCTCTCGTTCTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4761
15	Triazine Resistant D1 Protein <i>Hordeum vulgare</i> Ser264Thr AGT-ACT	CAGATTCTACTACAGGCCAAGCAGCCAAGAAGAAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGGCCACAATATTATAAGTCT	4762
		ATATGCT <u>ACT</u> TTCAACA	4763
		TGTTGAAAGTAGCATAT	4764
		AAACTTATAATATTGTGGCTGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCT <u>ACT</u> TTCAACAACCTCTCGTTCTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4765
		CAGATTCTACTACAGGCCAAGCAGCCAAGAAGAAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGGCCACAATATTATAAGTT	4766
20	Triazine Resistant D1 Protein <i>Triticum aestivum</i> Ser264Thr AGT-ACT	ATATGCT <u>ACT</u> TTCAACA	4767
		TGTTGAAAGTAGCATAT	4768
		AAACTTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTAATC TTCCAATATGCA <u>ACT</u> TTCAACAATTCTCGTTCTTACATTCTTCT AGCTGCTTGGCCTGTAGTAGGTATTG	4769
		CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAAGTT	4770
		ATATGCA <u>ACT</u> TTCAACA	4771
25	Triazine Resistant D1 Protein <i>Vigna unguiculata</i> Ser264Thr AGT-ACT	TGTTGAAAGTTGCATAT	4772

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Triazine Resistant D1 Protein <i>Lotus japonicus</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTCAACAACTCTCGTTCTTACACTCTTCT TAGCTGCTTGGCCTGTTGTAGGTATCTG	4773
	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACC GTGAGCAGCTACAATATTATAGGTTT	4774
	ATATGCAACTTCAACA	4775
	TGTTGAAAGTTGCATAT	4776
	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAAATTCTCGCTCTTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTG	4777
10 Triazine Resistant D1 Protein <i>Sinapis alba</i> Ser264Thr AGT-ACT	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACC GTGAGCAGCTACAATGTTGTAAGTTT	4778
	ATATGCTACTTCAACA	4779
	TGTTGAAAGTAGCATAT	4780
	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAAATTCTCGCTCTTACATTCTTCC TAGCTGCTTGGCCTGTTGTAGTAGGTATCTG	4781
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACC GTGAGCAGCTACAATATTATAGGTTT	4782
15 Triazine Resistant D1 Protein <i>Pisum sativum</i> Ser264Thr AGT-ACT	ATATGCTACTTCAACA	4783
	TGTTGAAAGTAGCATAT	4784
	AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGTCGATTGAT CTTCCAATATGCTACTTCAACAACTCTCGTTCTTACACTCTTCT TAGCTGCTTGGCCTGTTGTAGTAGGTATTG	4785
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGACCAAAAT AACC ATGAGCAGCTACGATATTATAAGTTT	4786
	ATATGCTACTTCAACA	4787
20 Triazine Resistant D1 Protein <i>Spinacia oleracea</i> Ser264Thr AGT-ACT	TGTTGAAAGTAGCATAT	4788
	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAACTCTCGTTCGTTACACTCTTCC TAGCTGCTTGGCCTGTTGTAGTAGGTATCTG	4789
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT TAACC ATGAGCAGCTACGATGTTATAAGTTT	4790
	ATATGCTACTTCAACA	4791
	TGTTGAAAGTAGCATAT	4792
25 Triazine Resistant D1 Protein <i>Nicotiana debneyi</i> Ser264Thr AGT-ACT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO
5 Triazine Resistant D1 Protein <i>Solanum nigrum</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTGGCCGATTGAT CTTCCAATATGCT <u>A</u> CTTCAACAACTCTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4793
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAGATCAATCGGCCAAA TAACCATGAGCGGCTACGATATTATAAGTT	4794
	ATATGCT <u>A</u> CTTCAACA	4795
	TGTTGAA <u>A</u> GTAGCATAT	4796
10 Triazine Resistant D1 Protein <i>Nicotiana</i> <i>plumbaginifolia</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTGGCCGATTGAT CTTCCAATATGCT <u>A</u> CTTCAACAACTCTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4797
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAGATCAATCGGCCAAA TAACCATGAGCGGCTACGATGTATAAGTT	4798
	ATATGCT <u>A</u> CTTCAACA	4799
	TGTTGAA <u>A</u> GTAGCATAT	4800

**Example 6**  
**Engineering male- or female-sterile plants**

Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, *AGAMOUS* (*AG*), *APETALA1* (*AP1*), and *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) in *Arabidopsis thaliana*, and *DEFICIENS A* (*DEFA*), *GLOBOSA* (*GLO*), *SQUAMOSA* (*SQUA*), and *PLENA* (*PLE*) in *Antirrhinum majus*. Genetic studies have shown that the *DEFA*, *GLO* and *AP3* genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

Altering the expression of these genes results in altered floral morphology. For example, mutations in *AP3* and *PI* result in male-sterile flowers because petals develop in place of stamens.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

**Table 14**  
**Oligonucleotides to produce male-sterile plants**

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile <i>AP3</i> <i>Arabidopsis thaliana</i> Arg3Term AGA-TGA	TTGCTCTCCACCAAATCTCTCAACAAAAAGATTAAACAAAGAGA GAAGAATATGGCGT <u>GAGGGAAGATCCAGATCAAGAGGATAGAGAA</u> CCAGACAAACAGACAAGTGA <u>CGTATTCAA</u>	4801
	TTGAATACGTC <u>ACTTGTCTGTCTGGTTCTATCCTCTTGATC</u> TGGATCTCCCT <u>CACGCCATATTCTCTCTCTTTGTTAATCTTTT</u> GTTGAAGAGATTGGTGGAGAGGACAA	4802
	ATATGGCGT <u>GAGGGAAG</u>	4803
	CTTCCCT <u>CACGCCATAT</u>	4804
Male-sterile <i>AP3</i> <i>Arabidopsis thaliana</i> Lys5Term AAG-TAG	TCTCCACCAAATCTCTCAACAAAAAGATTAAACAAAGAGAGAAGA ATATGGCGAGAGGG <u>TAGATCCAGATCAAGAGGATAGAGAACAGA</u> CAAACAGACAAGTGA <u>CGTATTCAAAGAGAA</u>	4805
	TTCTCTTGAATACGTC <u>ACTTGTCTGTCTGGTTCTATCCT</u> TTGATCTGGATCT <u>ACCCCTCGCCATATTCTCTCTTTGTTAAT</u> CTTTTGTTGAAGAGATTGGTGGAGA	4806
	CGAGAGGG <u>TAGATCCAG</u>	4807

	CTGGATCT <u>ACCCTCTG</u>	4808	
5	Male-sterile AP3 <i>Arabidopsis thaliana</i> Gln7Term CAG-TAG	CCAAATCTCTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG CGAGAGGGAAAGAT <u>CTAGATCAAGAGGATAGAGAACCAACAAACA</u> GACAAGTGA <u>CGTATTCAAAGAGAAGGAATG</u>	4809
		CATTCCCTCTCTTGAATACGTCACTTG <u>TGTCTGGTTCTCT</u> ATCCTCTTGAT <u>CTAGATCTCCCTCGCCATATTCTCTCTTTG</u> TTAATCTTTGTTGAAGAGATTGG	4810
		GGAAGAT <u>CTAGATCAAG</u>	4811
		CTTGAT <u>CTAGATCTCC</u>	4812
10	Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys9Term AAG-TAG	CTCTCAACAAAAAGATTAAACAAAGAGAGAAGAACCGAGAG GGAAGATCCAGAT <u>CTAGAGGATAGAGAACCAACAGACAAG</u> TGACGTATT <u>CAAAGAGAAGGAATGGTTAT</u>	4813
		ATAAACCATCCCTCTTGAATACGTCACTTG <u>TGTCTGGTTCTGG</u> TTCTCTATCCT <u>CTAGATCTGGATCTCCCTCGCCATATTCTCTC</u> TCTTGTTAATCTTTGTTGAAGAG	4814
		TCCAGAT <u>CTAGAGGATA</u>	4815
		TATCCT <u>CTAGATCTGG</u> A	4816
	Male-sterile AP3 <i>Brassica oleracea</i> Lys23Term AAG-TAG	AGAGGGAAAGATCCAGATCAAGAGGATAGAGAACCAACCGA CAAGTGACGTATT <u>CTTAGAGAAAGAAATGGTTGTTCAAGAAAGCTC</u> ACGAGCTTACAGTTTATGTGATGCTAGGG	4817
15		CCCTAGCATCACATAAAACTGT <u>AAAGCTCGTGAGCTTCTGAACAA</u> ACCATTCTCT <u>CTAAGAATACGTCACTTGTCGGTTGGTCTGGTTC</u> TCTATCCT <u>CTTGATCTGGATCTCCCTCT</u>	4818
		CGTATT <u>CTTAGAGAAGA</u>	4819
		TCTTCT <u>CTAAGAATACG</u>	4820
	Male-sterile AP3 <i>Brassica oleracea</i> Arg24Term AGA-TGA	GGGAAGATCCAGATCAAGAGGATAGAGAACCAACCGACAA GTGACGTATT <u>CTAAAGAAGAAATGGTTGTTCAAGAAAGCTCACG</u> AGCTTACAGTTTATGTGATGCTAGGGTT	4821
		AAACCCTAGCATCACATAAAACTGT <u>AAAGCTCGTGAGCTTCTTGAA</u> CAAACCATTCT <u>CTCACTTAGAATACGTCACTTGTCGGTTGGTCTGG</u> TTCTCTATCCT <u>CTTGATCTGGATCTCCCT</u>	4822
20		ATTCTAAG <u>CTGAAGAAAT</u>	4823
		ATTCT <u>CTCACTTAGAAT</u>	4824
	Male-sterile AP3 <i>Brassica oleracea</i> Arg25Term AGA-TGA	AAGATCCAGATCAAGAGGATAGAGAACCAACCGACAAAGTG ACGTATT <u>CTAAAGAGATGAAATGGTTGTTCAAGAAAGCTCACGAGC</u> TTACAGTTTATGTGATGCTAGGGTT <u>CGA</u>	4825
		TCGAAACCTAGCATCACATAAAACTGT <u>AAAGCTCGTGAGCTTCTT</u> GAACAAACCATT <u>CTAGAATACGTCACTTGTCGGTTGGTC</u> TGGTTCT <u>CTATCCTTGATCTGGATCTT</u>	4826
		CTAAGAG <u>ATGAAATGGT</u>	4827
25		ACCATT <u>CTAGTCTCTT</u> AG	4828

5	Male-sterile AP3 <i>Brassica oleracea</i> Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCAACCGACAAGTGACGTATTCTA AGAGAAGAAATGGTAGTTCAAGAAAGCTCACGAGCTTACAGTTT ATGTGATGCTAGGGTTCGATTATCATGTT	4829
		AACATGATAATCGAAACCCTAGCATCACATAAAACTGTAAGCTCGT GAGCTTCTTGAAC <u>T</u> AACCATTCTCTTAGAATACGTCACTTGT CGGTTGGCTGGTCTATCCTCTTGA	4830
		AAATGGTAGTTCAAGA	4831
		TCTTGAAC <u>T</u> AACCATT	4832
		GGCTCGAGGGAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGCAGGTACCTAG <u>T</u> CCAAGAGAACAGAAATGGTTGTTCAAGAA AGCACACGAGCTCTGTGTTCTGTGATGCT	4833
10	Male-sterile AP3 <i>Brassica napus</i> Tyr21Term TAC-TAG	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTTGAACAAACC ATTCTTCTTGG <u>A</u> CTAGGTGACCTGCCTGTTGTTGGTCTCTA TCCTCTTAATCTGGATCTCCCTCGAGCC	4834
		GTCACCTAG <u>T</u> CCAAGAG	4835
		CTCTTGG <u>A</u> CTAGGTGAC	4836
		CGAGGGAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGTACCTACTCCTAGAGAACAGAAATGGTTGTTCAAGAAAGCAC ACGAGCTCTGTGTTCTGTGATGCTAAAG	4837
		CTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTTGAACAA ACCATTCTCT <u>A</u> GGAGTAGGTGACCTGCCTGTTGTTGGTTC TCTATCCTCTTAATCTGGATCTCCCTCG	4838
15	Male-sterile AP3 <i>Brassica napus</i> Lys23Term AAG-TAG	CCTACTCCT <u>A</u> GAGAGAA	4839
		TCTTCTCT <u>A</u> GGAGTAGG	4840
		GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA GTCACCTACTCCAAG <u>T</u> GAAGAACAGAAATGGTTGTTCAAGAAAGCACACG AGCTCTCTGTGTTCTGTGATGCTAAAGTT	4841
		AAACTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTTGA CAAACCATTCT <u>C</u> ACTGGAGTAGGTGACCTGCCTGTTGTTGG TTCTATCCTCTTAATCTGGATCTCCC	4842
		ACTCCAAG <u>T</u> GAAGAAC ATTCTTCA <u>C</u> TTGGAGT	4843 4844
20	Male-sterile AP3 <i>Brassica napus</i> Arg24Term AGA-TGA	AAGATCCAGATTAAGAGGATAGAGAACCAAACAAA ACCTACTCCAAGAG <u>T</u> GAAGAACAGAAATGGTTGTTCAAGAAAGCACACGAGC TCTCTGTGTTCTGTGATGCTAAAGTTCCA	4845
		TGGAAACTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTT GAACAAACCATT <u>C</u> ACTCTGGAGTAGGTGACCTGCCTGTTGTT TGGTTCTCTATCCTCTTAATCTGGATCTT	4846
		CCAAGAG <u>T</u> GAAGAAC ACCATT <u>C</u> ACTCTGG	4847 4848

5	Male-sterile DEFA <i>Antirrhinum majus</i> Arg3Term CGA-TGA	GGAGAGAAAGGAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGT AGTGGTCGATGGCT <u>T</u> GAGGGAAAGATCCAGATTAAGAGGATAGAG AACCAAACAAACAGGCAGGTACCTACTCCA	4849
		TGGAGTAGGTGACCTGCCTGTTGGTTCTATCCTCTTAAT CTGGATCTCCCT <u>A</u> AGCCATCGAACCACTACCAACTGCTCTG TTTCTCTCCAGCTTCCTTCTCC	4850
		CGATGGCT <u>T</u> GAGGGAAAG	4851
		CTTCCCT <u>A</u> AGCCATCG	4852
		AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGG <u>T</u> AGATCCAGATTAAGAGGATAGAGAACAA ACAAACAGGCAGGTACCTACTCCAAGAGAA	4853
10	Male-sterile DEFA <i>Antirrhinum majus</i> Lys5Term AAG-TAG	TTCTCTGGAGTAGGTGACCTGCCTGTTGGTTCTATCCT CTTAATCTGGAT <u>T</u> ACCCCTCGAGCCATCGAACCACTACCAACTG CTCTGTTTCTTCCAGCTTCCTT	4854
		CTCGAGGG <u>T</u> AGATCCAG	4855
		CTGGAT <u>T</u> ACCCCTCGAG	4856
		AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTCGATG GCTCGAGGGAAAGAT <u>T</u> AGATTAAGAGGATAGAGAACAAACAAAC AGGCAGGTACCTACTCCAAGAGAAATG	4857
		CATTCTCTCTGGAGTAGGTGACCTGCCTGTTGGTTCTC TATCCTCTTAAT <u>T</u> AGATCTCCCTCGAGCCATCGAACCACTACCA CTACTGCTCTGTTCTTCCAGCTT	4858
15	Male-sterile DEFA <i>Antirrhinum majus</i> Gln7Term CAG-TAG	GGAAGAT <u>T</u> AGATTAAG	4859
		CTTAAT <u>T</u> AGATCTTCC	4860
		GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTCGATGGCTGA GGGAAGATCCAGATT <u>T</u> AGAGGATAGAGAACAAACAAACAGGCAG GTCACCTACTCCAAGAGAAAGAAATGGTTGT	4861
		ACAAACCATTTCTCTTGGAGTAGGTGACCTGCCTGTTGGTTG GTTCTCTATCCT <u>T</u> AAATCTGGATCTCCCTCGAGCCATCGAACCA CTACCAACTACTGCTCTGTTCTTCC	4862
		TCCAGATT <u>T</u> AGAGGATA	4863
20	Male-sterile DEFA <i>Antirrhinum majus</i> Lys9Term AAG-TAG	TATCCTCT <u>T</u> AAATCTGGGA	4864
		TCAGTAATTCTTAAGATCTCAA <u>T</u> TGAGCAAAAGAAAAAAAC TATGGCTCGTGGG <u>T</u> AGATCCAGATCAAGAGAATAGAGAACAAAC AAACAGACAAGTC <u>A</u> CTTATTCTAAGAGAA	4865
		TTCTCTTGAATAAGTGACTTGCTGTTGGTTCTCTATTCTC TTGATCTGGAT <u>T</u> ACCCACGAGCCATAGTTTTTTCTTTGCTC AAAGTTGAGATCTTAAGAATTACTGA	4866
		CTCGTGGG <u>T</u> AGATCCAG	4867
		CTGGAT <u>T</u> ACCCACGAG	4868
25	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys5Term AAG-TAG		

5	Male-sterile AP3 <i>Nicotiana tabacum</i> Gln7Term CAG-TAG	ATTCTTAAGATCTCAAACCTTGAGCAAAAAGAAAAAAACTATGGC TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAAACAAACAGA CAAGTCACTTATTCTAAGAGAAGAAATG	4869
		CATTCTCTCTTAAAGATAAGTGACTGTCTGTTGTTGGTCTCT ATTCTCTTGATCTAGATCTCCCACGAGCCATAGTTTTTTCTT TTGCTCAAAGTTGAGATCTAAGAAATG	4870
		GGAAGATCTAGATCAAG	4871
		CTTGATCTAGATCTCC	4872
10	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys9Term AAG-TAG	AAGATCTCAAACCTTGAGCAAAAAGAAAAAAACTATGGCTCGT GGAAGATCCAGATCTAGAGAATAGAGAACCAAACAAACAGACAAGT CACTTATTCTAAGAGAAGAAATGGACTTT	4873
		AAAGTCCATTCTCTCTTAAAGATAAGTGACTGTCTGTTGTTGG TTCTCTATTCTCTAGATCTGGATCTCCCACGAGCCATAGTTTTTT TTCTTTTGCTCAAAGTTGAGATCTT	4874
		TCCAGATCTAGAGAATA	4875
		TATTCTCTAGATCTGGA	4876
		ATCTCAAACCTTGAGCAAAAAGAAAAAAACTATGGCTCGTGGGA AGATCCAGATCAAGTGAATAGAGAACCAAACAAACAGACAAGTCAC TTATTCTAAGAGAAGAAATGGACTTTCA	4877
15	Male-sterile AP3 <i>Nicotiana tabacum</i> Arg10Term AGA-TGA	TGAAAAGTCCATTCTCTCTTAAAGATAAGTGACTGTCTGTTGTT TGGTTCTCTATTCACTTGATCTGGATCTCCCACGAGCCATAGTTT TTTTTCTTTTGCTCAAAGTTGAGAT	4878
		AGATCAAGTGAATAGAG	4879
		CTCTATTCACTTGATCT	4880
		GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA CAGACAAGTAACCTAGTCAAACCGAAGGGATGGTCTTTCAAGAAC GCCAATGAGCTCACTGTTCTTGATGCT	4881
		AGCATCACAAAGAACAGTGAGCTCATTGGCCTCTGAAAAGACCA TCCCTCGTTTGACTAAGTTACTTGCTGTTGTTGTCTAT TCTCTTGATCTGGATCTTCCTCGAGCC	4882
20	Male-sterile AP3 <i>Medicago sativa</i> Tyr21Term TAC-TAG	GTAACCTAGTCAAACG	4883
		CGTTTGACTAAGTTAC	4884
		CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA GACAAGTAACCTACTGAAAACCGAAGGGATGGTCTTTCAAGAAC CAATGAGCTCACTGTTCTTGATGCTAA	4885
		TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTCTGAAAAGAC CATCCCTCGTTTCAAGTTACTTGCTGTTGTTGTCT ATTCTCTTGATCTGGATCTTCCTCGAG	4886
		AACTTACTGAAAACGAA	4887
25	Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA	TTCGTTTCAAGTT	4888

5	Male-sterile AP3 <i>Medicago sativa</i> Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACCTACTCATAACGAAGGGATGGCTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTGTGATGCTAAGG	4889
		CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTGAAAAG ACCATCCCTCGTTATGAGTAAGTTACTGTCTGTTCGTTGTGTTCT CTATTCTCTGATCTGGATCTTCCTCG	4890
		CTTACTCATAACGAAGG	4891
		CCTTCGTTATGAGTAAG	4892
		GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACCTACTCAAAATGAAGGGATGGCTTTCAAGAAGGCCAATG AGCTCACTGTTCTTGTGATGCTAAGGTT	4893
10	Male-sterile AP3 <i>Medicago sativa</i> Arg24Term CGA-TGA	AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTGAA AAGACCATCCCTCATTTGAGTAAGTTACTGTCTGTTCGTTGTGTT TCTCTATTCTCTTGTGATCTGGATCTTCCTC	4894
		ACTCAAAATGAAGGGAT	4895
		ATCCCTTCATTTGAGT	4896
		GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTAGTCAAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACCTACAGTTCTTGTGATGCT	4897
		AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTGAATAGCCA TTCTTCTCTTGTGACTAAGTCACTTGCCTATTGTTGGTTTCTATT TTCTTGATCTGGATCTTACACACGAGCC	4898
15	Male-sterile DEF4 <i>Solanum tuberosum</i> Tyr21Term TAT-TAG	GTGACTTAGTCAAAAGAG	4899
		CTCTTGACTAAGTCAC	4900
		CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATTGAAAGAGAAGAAATGGGCTATTCAAGAAGGCT AATGAACCTACAGTTCTTGTGATGCTAA	4901
		TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTGAATAGCC CATTCTCTCTTCAATAAGTCACTTGCCTATTGTTGGTTTCTA TTTCTTGATCTGGATCTTACACACGAG	4902
		GACTTATTGAAAGAGAA	4903
20	Male-sterile DEF4 <i>Solanum tuberosum</i> Ser22Term TCA-TGA	TTCTCTTCAATAAGTC	4904
		CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGC AAGTGACTTATTCATAGAGAAGAAATGGGCTATTCAAGAAGGCTAA TGAACCTACAGTTCTTGTGATGCTAAAG	4905
		CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTGAATAGC CCATTCTCTCTATGAATAAGTCACTTGCCTATTGTTGGTTTCTC TATTCTTGATCTGGATCTTACACACG	4906
		CTTATTCAAGAGAAGA	4907
		TCTCTCTATGAATAAG	4908
25	Male-sterile DEF4 <i>Solanum tuberosum</i> Lys23Term AAG-TAG		

5	Male-sterile DEF4 <i>Solanum tuberosum</i> Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAAACAATAGGCAAG TGACTTATTCAAAGTGAAGAAATGGCTATTCAAGAAGGCTAATGA ACTTACAGTTCTTGTGATGCTAAAGTT	4909
		AAACTTTAGCATCACAAAGAACTGTAAGTTCAATTGCCTCTTGAAT AGCCCATTTCTTCACTTGAATAAGTCACTTGCCTATTGTTGGTT	4910
		TTCTATTTCCTGATCTGGATCTTACCC	
		ATTCAAAGTGAAGAAAT	4911
		ATTTCCTTCACTTGAAT	4912
10	Male-sterile AP3 <i>Lycopersicon esculentum</i> Gly27Term GGA-TGA	GCTAATGAACCTACTGTTCTTGTGATGCTAAAGTTCAATTGTTAT GATTCTAGTACTTGAAGAAACTTCAATTGTTGATGCTTATAAGTCCCTATCA CGACCAAAACAATTGTTGATCTGTAC	4913
		GGTACAGATCGAACAAATTGTTGGTCGTGATAGAGGGACTTATAAA CTCATGAAGTTTCAAGTACTAGAAATCATAACAATTGAAACTTAG	4914
		CATCACAAAGAACAGTAAGTTCAATTGTTGATCTGTAC	
		CTAGTACTTGAAGAAACTT	4915
		AAGTTTCAAGTACTAG	4916
15	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys28Term AAA-TAA	AATGAACCTACTGTTCTTGTGATGCTAAAGTTCAATTGTTATGAT TTCTAGTACTGGATAACTTCAATTGTTGATGCTTATAAGTCCCTATCACGA CCAAACAATTGTTGATCTGTAC	4917
		TCTGGTACAGATCGAACAAATTGTTGGTCGTGATAGAGGGACTTAT AAACTCATGAAGTTATCCAGTACTAGAAATCATAACAATTGAAACTT	4918
		TAGCATCACAAAGAACAGTAAGTTCAATTGTTGATCTGTAC	
		GTACTGGATAACTTCAT	4919
		ATGAAGTTATCCAGTAC	4920
20	Male-sterile AP3 <i>Lycopersicon esculentum</i> Glu31Term GAG-TAG	ACTGTTCTTGTGATGCTAAAGTTCAATTGTTATGATTCTAGTAC TGGAAAACCTTCATTAGTTATAAGTCCCTATCACGACCAAACAAT TGTTGATCTGTACAGAAGACTATTG	4921
		CAATAGTCTTCTGGTACAGATCGAACAAATTGTTGGTCGTGATAGA GGGACTTATAAACTAATGAAGTTTCACTAGAAATCATAACAA	4922
		TTGAAACTTAGCATCACAAAGAACAGT	
		AACTTCATTAGTTATA	4923
		TATAAACTAATGAAGTT	4924
25	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys40Term AAA-TAA	ATTGTTATGATTCTAGTACTGGAAAACCTTCATGAGTTATAAGTCC CTCTATCACGACCTAACATTGTTGATCTGTACCAAGAAGACTATT GGAGTTGATATTGGACTACTCACTATG	4925
		CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTGGTACAG ATCGAACAAATTGTTAGGTCGTGATAGAGGGACTTATAAACTCATGA	4926
		AGTTTCCAGTACTAGAAATCATAACAA	
		TCACGACCTAACATTG	4927
		CAATTGTTAGGTCGTGA	4928

5	Male-sterile AP3 <i>Triticum aestivum</i> Tyr21Term TAC-TAG	GGGGCGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCTAGTCCAAGCGCCGGTCGGGGATCATGAAG AAGGCGCGGGAGCTCACCGTGCTCTGCAGCGCC	4929	
		GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTCTTCATGATCC CCGACCGCGCTTGGACTAGGTACACTGCCTGTTGGTGGCGTTC TCGATCCGCTTATCTCAATCTCCCCGCC	4930	
		GTGACCTAGTCCAAGCG	4931	
		CGCTTGGACTAGGTAC	4932	
	Male-sterile AP3 <i>Triticum aestivum</i> Lys23Term AAG-TAG	CGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGACCTACTCCTAGCGCCGGTCGGGGATCATGAAGAAGG CGCGGGAGCTCACCGTGCTCTGCAGCGCC	4933	
10		CCTGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTCTTCATG ATCCCCGACCGGGCGCTAGGAGTAGGTACACTGCCTGTTGGTGGC GTTCTCGATCCGCTTATCTCAATCTCCCCG	4934	
		CCTACTCCTAGCGCCGG	4935	
		CCGGCGCTAGGAGTAGG	4936	
		TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACTCCAAGCGCCGGTAGGGATCATGAAGAAGGCGCGGGAGCTC ACCGTGCTCTGCAGCGCCAGGTGCCATCAT	4937	
15	Male-sterile AP3 <i>Triticum aestivum</i> Ser26Term TCG-TAG	ATGATGGCGACCTGGCGTCGCAGAGCACGGTGAGCTCCCGCGC CTTCTCATGATCCCCCTACCGCGCTTGGAGTAGGTACACTGCCT GTTGGTGGCGTCTCGATCCGCTTATCTCAA	4938	
		GCGCCGGTAGGGATCA	4939	
		TGATCCCCTACCGGGCGC	4940	
		CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG CCGGTCGGGGATCATGTAGAAGGCGCGGGAGCTCACCGTGCTCT GCGACGCCAGGTGCCATCATCATGTTCTCCT	4941	
		AGGAGAACATGATGATGGCGACCTGGCGTCGCAGAGCACGGTG AGCTCCCGCGCCTCTACATGATCCCCGACCGGGCGCTGGAGTA GGTCACCTGCCTGTTGGTGGCGTCTCGATCCG	4942	
20	Male-sterile AP3 <i>Triticum aestivum</i> Lys30Term AAG-TAG	GGATCATGTAGAAGGCG	4943	
		CGCCTTCTACATGATCC	4944	
		GGGGCGGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA ACCGCCAGGTGACCTAGTCCAAGCGCCGGACGGGGATCATGAAG AAGGCACCGCGAGCTCACCGTGCTCTGCAGCGCC	4945	
		GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTCTTCATGATCC CCGTCGGCGCTTGGACTAGGTACACTGGCGGTTGGTGGCGTTC TCGATCCGCTTGTCTCGATCTGCCGCC	4946	
		GTGACCTAGTCCAAGCG	4947	
25	Male-sterile Silky1 <i>Zea mays</i> Tyr21Term TAC-TAG	CGCTTGGACTAGGTAC	4948	

5	Male-sterile Silky1 <i>Zea mays</i> Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCCTAGCGCCGGACGGGGATCATGAAGAACGG CACCGAGCTCACCCTGCTCTGCACGCCAGG	4949
		CCTGGCGTCGCAGAGCACGGTAGCTCGCTGCCTCTCATG ATCCCCGTCGGCGCTAGGAGTAGGTCACCTGGCGGTTGGTGGC GTTCTCGATCCGCTTGTATCTCGATCTGCCGCG	4950
		CCTACTCCTAGCGCCGG	4951
		CCGGCGCTAGGAGTAGG	4952
10	Male-sterile Silky1 <i>Zea mays</i> Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATGTAGAAGGCACCGAGCTCACCGTGCTCT GCGACGCCAGGTGCCATCATCATGTTCTCCT	4953
		AGGAGAACATGATGATGGCGACCTGGCGTCGCAGAGCACGGT AGCTCGCGTGCCTCTACATGATCCCCGTCCGGCGCTGGAGTAG GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	4954
		GGATCATGTAGAAGGCA	4955
		TGCCTTCTACATGATGCC	4956
		ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAGTAGGCACCGAGCTCACCGTGCTCTCGC ACGCCAGGTGCCATCATCATGTTCTCCTCCA	4957
15	Male-sterile Silky1 <i>Zea mays</i> Lys31Term AAG-TAG	TGGAGGAGAACATGATGATGGCGACCTGGCGTCGCAGAGCACG GTGAGCTCGCGTGCCTACTCATGATCCCCGTCCGGCGCTTGG GTAGGTACCTGGCGGTTGGTGGCGTTCTCGAT	4958
		TCATGAAGTAGGCACGC	4959
		GGGTGCCTACTCATGA	4960
		GCTAGCTGCATTGTCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAAGCGCC	4961
20	Male-sterile AP3 <i>Oryza sativa</i> Lys5Term AAG-TAG	GGCGCTTCGAGTAGGTACCTGCCTGTTGGTCGCCTCTCGATCC GCTTGATCTCGATCTAGCCCCCTCCCATGGCCGCCCCCTGCAGC AGCTATCTCTCGCCGGACAATGCAGCTAGC	4962
		GGAGGGGCTAGATCGAG	4963
		CTCGATCTAGCCCCCTCC	4964
		TGCATTGTCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACCGCACCA ACAGGCAGGTGACCTACTCGAAGCGCCGACCG	4965
		CCGTGCGCGCTTCGAGTAGGTACCTGCCTGTTGGTCGCCTCT CGATCCGCTTGTATCTAGATCTTGCCTCCCATGGCCGCCCCCT GCAGCAGCTATCTCTCGCCGGACAATGCA	4966
25	Male-sterile AP3 <i>Oryza sativa</i> Glu7Term GAG-TAG	GCAAGATCTAGATCAAG	4967
		CTTGATCTAGATCTTGC	4968

5	Male-sterile AP3 <i>Oryza sativa</i> Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGA GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAACGCGCCACGGGATCA	4969
		TGATCCCCGTGCGCGCTTCGAGTAGGTACCTGCCTGTTGGTC GCGTTCTCGATCCGCTAGATCTCGATCTGCCCTCCCCATGGCC GCCCCCTGCAGCAGCTATCTCTCGCCGGAC	4970
		TCGAGATCTAGCGGATC	4971
		GATCCGCTAGATCTCGA	4972
10	Male-sterile AP3 <i>Oryza sativa</i> Glu12Term GAG-TAG	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGAGGGGCAAGA TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT ACTCGAACGCGCCACGGGATCATGAAGAAGG	4973
		CCTTCTTCATGATCCCCGTGCGCGCTTCGAGTAGGTACCTGCC TGTTGGTCGCGTTCTAGATCCGCTTGATCTCGATCTGCCCTCC CCATGGCCGCCCTGCAGCAGCTATCTCTC	4974
		AGCGGATCTAGAACGCG	4975
		CCGCTTCTAGATCCGCT	4976

Table 15  
Oligonucleotides to produce male-sterile plants

15	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
20	Male-sterile AG <i>Arabidopsis thaliana</i> Tyr35Term TAC-TAG	TCGTACTAATCAAATTGCCCTAACGTTTGGCTTGGAGCA GCAATCACGGCGTAGCAATCGGAGCTAGGAGGGAGATTCCCTCTCC CTTGAGGAAATCTGGAGAGGAAAGATCGAA	4977
		TTCGATCTTCCTCTCCAGATTCCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAA ACGTTAGGGCAAAATTGATTAGTACAGA	4978
		ACGGCGTAGCAATCGGA	4979
		TCCGATTGCTACGCCGT	4980
		CTGTACTAATCAAATTGCCCTAACGTTTGGCTTGGAGCAG CAATCACGGCGTAGCAATCGGAGCTAGGAGGGAGATTCCCTCCCT TGAGGAAATCTGGAGAGGAAAGATCGAAA	4981
25	Male-sterile AG <i>Arabidopsis thaliana</i> Gln36Term CAA-TAA	TTTCGATCTTCCTCTCCAGATTCCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAA AACGTTAGGGCAAAATTGATTAGTACAG	4982
		CGGGCGTAGCAATCGGAG	4983
		CTCCGATTAGTACGCCG	4984

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile AG <i>Arabidopsis thaliana</i> Ser37Term TCG-TAG	ACTAATCAAATTTGCCCTAACGTTTGGCTTGGAGCAGCAAT CACGGCGTACCAAT <u>AGGAGCTAGGAGGAGATTCCCTCCCTTGA</u> GGAAATCTGGGAGAGGAAGATCGAAATCAA	4985
		TTGATTCGATCTTCCTCTCCCAGATTCCTCAAGGGAGAGGAAT CTCCTCCTAGCTCTATTGGTACGCCGTATTGCTGCTCCAAAGC CAAAAACGTTAGGGAAAATTGATTAGT	4986
		GTACCAAT <u>AGGAGCTAG</u>	4987
		CTAGCTCTATTGGTAC	4988
10	Male-sterile AG <i>Arabidopsis thaliana</i> Glu38Term GAG-TAG	TAATCAAATTTGCCCTAACGTTTGGCTTGGAGCAGCAATCA CGGCGTACCAATCG <u>TAGCTAGGAGGAGATTCCCTCCCTGAGGA</u> AATCTGGGAGAGGAAGATCGAAATCAAAC	4989
		GTITGATTCGATCTTCCTCTCCCAGATTCCTCAAGGGAGAGGA ATCTCCTCCTAGCT <u>ACGATTGGTACGCCGTATTGCTGCTCCAA</u> GCCAAAAACGTTAGGGAAAATTGATTA	4990
		ACCAATCG <u>TAGCTAGGA</u>	4991
		TCCTAGCT <u>ACGATTGGT</u>	4992
		CTCTCCCACTTCTTTCGGTGGTTATTCAATTGGTACGATATCA CAGAAGCAATGGAT <u>TAAGGTGGGAGTAGTCACGATGCAGAGAGTA</u> GCAAGAAGATAGGTAGAGGGAAAGATAGAGA	4993
15	Male-sterile AG <i>Brassica napus</i> Glu3Term GAA-TAA	TCTCTATCTCCCTACCTATCTTCTGCTACTCTGCATCGT ACTACTCCCACCTT <u>AATCCATTGCTTCTGTGATATCGTCACCAAAT</u> GAATAAACCAACCGAAAAGAAGTGGGAGAG	4994
		CAATGGAT <u>TAAGGTGGG</u>	4995
		CCCACCTT <u>AATCCATTG</u>	4996
		TATTCATTGGTACGATATCACAGAACGAAATGGATGAAGGTGGG AGTAGTCACGATGC <u>ATAGAGTAGCAAGAACAGATAGGTAGAGGGAAAG</u> ATAGAGATAAAGAGGGATAGAGAACACAACAA	4997
		TTGTTGTCTCTATCCTTATCTCTATCTTCCCTACCTATC TTCTGCTACTCT <u>ATGCATCGTACTACTCCCACCTTCATCCATTG</u> CTTCTGTGATATCGTCACCAAATGAATA	4998
20	Male-sterile AG <i>Brassica napus</i> Glu11Term GAG-TAG	ACGATGC <u>ATAGAGTAGC</u>	4999
		GCTACTCT <u>ATGCATCGT</u>	5000
		GGTGACGATATCACAGAACGAAATGGATGAAGGTGGGAGTAGTCA CGATGCAGAGAGTAGCT <u>AGAACAGATAGGTAGAGGGAAAGATAGAGAT</u> AAAGAGGGATAGAGAACACAACAAATCGTCAAG	5001
		CTTGACGATTGGTGTCTATCCTCTTATCTCTATCTTCCCT CTACCTATCTCT <u>AGCTACTCTGCATCGTACTACTCCCACCTT</u> CATCCATTGCTTCTGTGATATCGTCACC	5002
		AGAGTAG <u>CTAGAACAGATA</u>	5003
25	Male-sterile AG <i>Brassica napus</i> Lys14Term AAG-TAG	TATCTTCT <u>AGCTACTCT</u>	5004

	Phenotype, Gene Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile AG <i>Brassica napus</i> Lys15Term AAG-TAG	GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGAT GCAGAGAGTAGCAAGTAGATAGGTAGAGGGAAAGATAGAGATAAAG AGGATAGAGAACACAACAAATCGTCAAGTAA	5005
		TTACTTGACGATTGTTGTCTCTATCCTCTTATCTCTATCTTC CCTCTACCTATCTACTTGCTACTCTCGCATCGTACTACTCCCAC CTTCATCCATTGCTCTGTGATATCGTC	5006
		GTAGCAAGTAGATAGGT	5007
		ACCTATCTACTTGCTAC	5008
10	Male-sterile AG <i>Lycopersicon esculentum</i> Glu4Term CAA-TAA	CAACCAAAAACCTAAAAATCTTCTCTTCCCTTACAAGGTGA AGTAATGGACTCTAAAGTGTCTAACCCAGAGAGATCTCACCAAA AGGAAACTAGGAAGGGGGAAAATTGAGA	5009
		TCTCAATTTCCTCCCTAGTTCCCTTGAGATCTCTCT GGTTAGATCACTT <del>A</del> GAAGTCCATTACTCACCTTGAAGGAAAGG AAAGAGAAGATTTAAGTTTTGGTTG	5010
		TGGACTTCT <del>A</del> AAAGTGTAT	5011
		ATCACTT <del>A</del> GAAGTCCA	5012
15	Male-sterile AG <i>Lycopersicon esculentum</i> Arg9Term AGA-TGA	AAAATCTTCTCTTCCCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAACCT <del>G</del> GAGAGATCTCACCAAAAGGAAACTAGGAA GGGGGAAAATTGAGATCAAAAGGATCGAAA	5013
		TTTCGATCCTTGTATCTCAATTTCCTCCCTAGTTCCCTTGT GGTGAGATCTCTC <del>A</del> GGTTAGATCACTTGGAAAGTCCATTACTCAC CTTGTAAAGGAAAGGAAAGAGAAGATT	5014
		ATCTAACCT <del>G</del> GAGAGATC	5015
		GATCTCTC <del>A</del> GGTTAGAT	5016
20	Male-sterile AG <i>Lycopersicon esculentum</i> Glu10Term GAG-TAG	ATCTTCTCTTCCCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAACAGATAGATCTCACCAAAAGGAAACTAGGAAGGG GGAAAATTGAGATCAAAAGGATCGAAAACA	5017
		TGTTTCGATCCTTGTATCTCAATTTCCTCCCTAGTTCCCTT TGTGGTGAGATCT <del>A</del> CTGGTTAGATCACTTGGAAAGTCCATTACT CACCTTGTAAAGGAAAGGAAAGAGAAGAT	5018
		TAACCAGATAGATCTCA	5019
		TGAGATCT <del>A</del> CTGGTTA	5020
25	Male-sterile AG <i>Lycopersicon esculentum</i> Ser12Term TCA-TGA	CTTCCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGTACT AACCAGAGAGATCT <del>G</del> ACCACAAAGGAAACTAGGAAGGGGGAAAAT TGAGATCAAAAGGATCGAAAACACGACGAA	5021
		TTCGTCGTGTTCGATCCTTGTATCTCAATTTCCTCCCTA GTTCCTTGTGGT <del>C</del> AGATCTCTGGTTAGATCACTTGGAAAGTC CATTACTCACCTTGTAAAGGAAAGGAAAG	5022
		AGAGATCT <del>G</del> ACCACAA	5023

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTTGTGGTC <u>CAGATCTCT</u>	5024
5 Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln4Term CAA-TAA	GTACTCTCTATTTCATCTTCCAACCCCTTCTTCCCTTACCAAGGTGA AAGTATGGACTT <u>C</u> AAAGTGATCTAACAAAGAGAGATCTCTCCACAA AGGAAACTGGAAAGAGGAAAGATTGAGA	5025
	TCTCAATCTTCCCTTCCCAGTTCTTGTGGAGAGATCTCTCT TGTTAGATCACTT <u>A</u> GAAGTCCATACTTACCTGGTAAGGAAAGA	5026
	TGGACTT <u>C</u> AAAGTGAT	5027
	ATCACTT <u>A</u> GAAGTCCA	5028
10 Male-sterile NAG1 <i>Nicotiana tabacum</i> Arg9Term AGA-TGA	ATCTTCCAACCCCTTCTTCCCTTACCAAGGTGAAGATGGACTTCC AAAGTGATCTAACAT <u>G</u> AGAGAGATCTCTCCACAAAGGAAACTGGGAA GAGGAAAGATTGAGATCAAACGGATCGAAA	5029
	TTCGATCCGTTGATCTCAATCTTCCCTTCCCAGTTCTTGT GGAGAGATCTCT <u>C</u> ATGTTAGATCACTTGGAAAGTCCATACTTAC CTGGTAAGGAAAGAAAGGGTTGGAAAGAT	5030
	ATCTAACAT <u>G</u> AGAGATC	5031
	GATCTCT <u>C</u> ATGTTAGAT	5032
	TTCCAACCCCTTCTTCCCTTACCAAGGTGAAGATGGACTTCCAAA GTGATCTAACAA <u>G</u> ATAGATCTCTCCACAAAGGAAACTGGGAGAG GAAAGATTGAGATCAAACGGATCGAAAACA	5033
15 Male-sterile NAG1 <i>Nicotiana tabacum</i> Glu10Term GAG-TAG	TGTTTCGATCCGTTGATCTCAATCTTCCCTTCCCAGTTCTT TGTGGAGAGATCT <u>A</u> CTTGTAGATCACTTGGAAAGTCCATACTT CACCTGGTAAGGAAAGAAAGGGTTGGAA	5034
	TAACAAG <u>G</u> ATAGATCTCT	5035
	AGAGATCT <u>A</u> CTTGTAA	5036
	CTTCCCTTACCAAGGTGAAGATGGACTTCCAAAGTGATCTAACAA GAGAGATCTCC <u>C</u> ATAAGGAAACTGGGAGAGGAAAGATTGAGA TCAAACGGATCGAAAACACAACGAATCGTC	5037
	GACGATT <u>C</u> GTTGTGTTCGATCCGTTGATCTCAATCTTCCCT TCCCAGTTCTT <u>A</u> TGGAGAGATCTCTCTTGTAGATCACTTGG AAGTCCATACTTACCTGGTAAGGAAAG	5038
20 Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln14Term CAA-TAA	TCTCTCC <u>C</u> ATAAGGAAAG	5039
	TTTCCTT <u>A</u> TGGAGAGA	5040
	GCCTATGAAAACAACCCAAACACGGCTGGACGCTGATGCCAA AGAAGATTGGGAAGGT <u>G</u> AAAGATCGAGAGATCAAGCGGATCGAAAAC ACCACCAATCGTCAAGTCACCTCTGCAAAA	5041
	TTTGCAGAAGGTGACTTGACGATTGGTGGTGT <u>T</u> CGATCCGCT TGATCTCGATCTT <u>C</u> ACCTCCCAATCTCTTGGGCATCAGCGTC CAGGACCGTGTGGTTGT <u>C</u> ATAGGC	5042
	TGGGAAGGT <u>G</u> AAAGATC	5043
25 Male-sterile AG <i>Rosa hybrida</i> Gly22Term GGA-TGA	GATCTT <u>C</u> ACCTCCCA	5044

	Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile AG <i>Rosa hybrida</i> Lys23Term AAG-TAG	TATGAAAACAAACCAACACGGTCCTGGACGCTGATGCCAAAGA AGATTGGGAAGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTCTGCAAAGGC	5045
		GCCTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCC GCTTGATCTCGATCTAGATCCCCTCCCAATCTTCTTGGGCATCAGC GTCCAGGACCGTGTGGTTGGTTCTATA	5046
		GAAGGGGATAGATCGAG	5047
		CTCGATCTATCCCCCTC	5048
10	Male-sterile AG <i>Rosa hybrida</i> Glu25Term GAG-TAG	AACAAACCCAACACGGTCCTGGACGCTGATGCCAAAGAAGATTG GGAAGGGGAAAGATCTAGATCAAGCGGATCGAAAACACCAAT CGTCAAGTCACCTCTGCAAAGGCAGCAATG	5049
		CATTGCGCTTTGCAGAAGGTGACTTGACGATTGGTGGTGT CGATCCGCTTGTATCTAGATCTTCCCCTCCCAATCTTCTTGGC ATCAGCGTCCAGGACCGTGTGGTTGTT	5050
		GAAAGATCTAGATCAAG	5051
		CTTGATCTAGATCTTC	5052
		CCCAACACGGTCCTGGACGCTGATGCCAAAGAAGATTGGGAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCAATCGTCA AGTCACCTCTGCAAAGGCAGCAATGGTTGC	5053
15	Male-sterile AG <i>Rosa hybrida</i> Lys27 AAG-TAG	GCAAACCATTCGCGCTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTTCGATCCGCTAGATCTGATCTTCCCCTCCCAATCTTCT TTGGGCATCAGCGTCCAGGACCGTGTGGGG	5054
		TCGAGATCTAGCGGATC	5055
		GATCCGCTAGATCTCGA	5056
		CAATTGCTGTTTATTTTTCTTTTGACTAAGTAGAAATGGC GTCTCTAAGCGATTAATCGACCGAGGTATGCCCGAGAGGAAAT CGGGAGAGGAAAGATCGAGATCAAACCGGA	5057
		TCCGTTGATCTCGATCTTCTCTCCGATTTCCTCTCGGGCGA TACCTCGGTCGATTAAATCGCTTAGAGACGCCATTCTACTTAGTCA AAAAGAAAAAAAATAAAAACAGGCAATTG	5058
20	Male-sterile far <i>Antirrhinum majus</i> Gln7Term CAA-TAA	TAAGCGATTAATCGACC	5059
		GGTCGATTAATCGCTTA	5060
		GTTTTTATTTTTCTTTTGACTAAGTAGAAATGGCGTCTCTAAG CGATCAATCGACCTAGGTATCGCCCGAGAGGAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA	5061
		TGTTTCGATCCGTTGATCTCGATCTTCTCTCCGATTTCCT CTCGGGCGATACCTAGGTCGATTGATCGCTTAGAGACGCCATT TACTTAGTCAAAAAGAAAAAAAATAAAAAC	5062
		AATCGACCTAGGTATCG	5063
25	Male-sterile far <i>Antirrhinum majus</i> Glu10Term GAG-TAG	CGATACCTAGGTCGATT	5064

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile far <i>Antirrhinum majus</i> Glu14Term GAG-TAG	TTCTTTGACTAAGTAGAAATGGCGTCTCTAACGCGATCAATCGA CCGAGGTATGCCCTAGAGGAAAATCGGGAGAGGAAAGATCGAG	5065
	ATCAAACGGATCGAAAACAAACAAATCAAC GTTGATTTGTTTGTTCGATCCGTTGATCTCGATCTTCCTCTC CCGATTTCCCTCTAGGGCGATACCTCGGTCGATTGATCGCTTAGA	5066
	GACGCCATTTCTACTTAGTCAAAAGAAA TATGCCCTAGAGGAAA	5067
	TTTCCTCTAGGGCGATA	5068
10 Male-sterile far <i>Antirrhinum majus</i> Lys16Term AAA-TAA	TTGACTAAGTAGAAATGGCGTCTCTAACGCGATCAATCGACCGAG GTATGCCCGAGAGGTAAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAACAAATCAACAGGGTA	5069
	TAACCTGTTGATTTGTTTGTTCGATCCGTTGATCTCGATCTT CCTCTCCGATTACCTCTCGGGCGATACCTCGGTCGATTGATCG CTTAGAGACGCCATTCTACTTAGTCAAA	5070
	CCGAGAGGTAAATCGGG	5071
	CCCGATTACCTCTCGG	5072
	Male-sterile AG <i>Cucumis sativus</i> Leu21Term TTG-TAG	5073
15 TTCTCTGAGGCAGTCTGACATCTCTCTTGATTCTGGAAACA TCCCCCTTATTGCTACTTACCCCTTCCTCTCCCTTAATCATTCTT GTGAGTGGTGAUTGATAATGCTTGGACA GGGTAAGTAGCAAATAA	TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA AGGAAAGGGTAAGTAGCAAATAAAGGGGATGTTCCAGAAATCAAGA AGAGAAGATGTCAGACTCGCCTCAGAGGAA	5074
	TTATTTGCTACTTACCC	5075
	TTATTTGCTACTTACCC	5076
	TTCTCCTCTGAGGCAGTCTGACATCTCTCTTGATTCTGGAA CATCCCCCTTATTGCTACTTACCCCTTCCTCTCCCTTAATCATTCT TTGTGAGTGGTGAUTGATAATGCTTGGACA	5077
20 GTAAGTTGTTAAATAAAG CTTTATTACAACTTAC	GAAAGGGTAAGTTGAAATAAAGGGGATGTTCCAGAAATCAAGAAG AGAAGATGTCAGACTCGCCTCAGAGGAA	5078
	GTAAGTTGTTAAATAAAG	5079
	CTTTATTACAACTTAC	5080
	CTTTATTACAACTTAC	5081
25 TTCCCCTTCTGAGGCAGTCTGACATCTCTCTTGATTCTGGAA CTGGAACATCCCCCTATTGCTACTTACCCCTTCCTCTCCCTTA ATCATTCTGTGAGTGGTGAUTGATAATG TGCAAATAAGGGGATG	CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG GGTAAGTTGCAAATAAGGGGATGTTCCAGAAATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAAGATGGGAA	5082
	CATCCCCTTATTGCTACTTACCCCTTCCTCTCCCTTA ATCATTCTGTGAGTGGTGAUTGATAATG	5083
	CATCCCCTTATTGCTACTTACCCCTTCCTCTCCCTTA ATCATTCTGTGAGTGGTGAUTGATAATG	5084

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG <i>Cucumis sativus</i> Gln28Term CAG-TAG	CCACTCACAGAATGATTAAGGAAGAAGGAAAGGGTAAGTTGCAA ATAAAGGGGATGTTCTAGAATCAAGAAGAGAAGATGTCAGACTCG CCTCAGAGGAAGATGGGAAGAGGAAAGATTG	5085
	CAATCTTCCTCTCCCATCTCCTCTGAGGGGAGTCTGACATCTT CTCTTCTTGATTCTAGAACATCCCCTTATTTGCAACTTACCCCTTC	5086
	CTTCTTCCTTAATCATTCTGTGAGTGG	
	GGATGTTCTAGAACATCAA	5087
	TTGATTCTAGAACATCC	5088
Male-sterile AG <i>Zea mays</i> Cys10Term TGC-TGA	CCACCACCACCAACCACACCACACCATGCTAACATGAT GAUTGATCTGAGCTGAGGGCCGTGTCAGGTCAAGGAGCAGG TGGCGGCCGCGCCGACGGGCTCCGGCGACAGG	5089
	CCTGTCGCCGGAGCCCGTCGGCGCCGCCACCTGCTCCTG ACCTGGACGACGGCCCTAGCTCAGATCAGTCATCATGTTGAGC ATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	5090
	CTGAGCTGAGGGCCGTC	5091
	GACGGCCCTCAGCTCAG	5092
Male-sterile AG <i>Zea mays</i> Ser13Term TCG-TAG	ACCACCACCAACCACACCACACCATGCTAACATGATGACTGATC TGAGCTGCGGGCCGTAGTCCAAGGTCAAGGAGCAGGTGGCGGC GGCGCCGACGGGCTCCGGCGACAGGCAGGGCA	5093
	TGCCCCTGCCCTGTCGCCGGAGCCCGTCGGCGCCGCCACCT GCTCCTTGACCTTGGACTACGGCCCGAGCTCAGATCAGTCATCA TGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	5094
	CGGGCCGTAGTCCAAGG	5095
	CCTTGGACTACGGCCCG	5096
Male-sterile AG <i>Zea mays</i> Lys15Term AAG-TAG	CACCAACCACCAACCACACCATGCTAACATGATGACTGATCTGAGC TGCGGGCCGTGTCCTAGGTCAAGGAGCAGGTGGCGGGCGC CGACGGGCTCCGGCGACAGGCAGGGCAGGGGA	5097
	TCCCCTGCCCTGCCCTGTCGCCGGAGCCCGTCGGCGCCGCC CACCTGCTCCTTGACCTAGGACGACGGCCCGCAGCTCAGATCAG TCATCATGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGT	5098
	CGTCGTCTAGGTCAAG	5099
	CTTGACCTAGGACGACG	5100
Male-sterile AG <i>Zea mays</i> Lys17Term AAG-TAG	CACCAACCACCAACCACACCATGCTAACATGATGACTGATCTGAGCTGGGG CCGTCGTCCAAGGTCTAGGAGCAGGTGGCGGGCGCCGACGG GCTCCGGCGACAGGCAGGGCAGGGGAGAGGGCA	5101
	TGCCTCTCCCCCTGCCCTGCCCTGTCGCCGGAGCCCGTCGGCGC CGCCGCCACCTGTCCTAGACCTTGGACGACGGCCCGCAGCTCA GATCAGTCATCATGTTGAGCATGGTGTGGTGGTGGTGGT	5102
	CCAAGGTCTAGGAGCAG	5103
	CTGCTCCTAGACCTTGG	5104

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile AG <i>Zea mays</i> Arg4Term CGA-TGA	TCCTACCTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATCT <u>GAGAAGAGGAGG</u> CTACACCACAGTAA CAGGCATCATGTCGACCTGACTTCGGCGG	5105
		CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTC <u>CAGATGTG</u> CATGCTCTGTTCCATCACACA GATTTGAGGTCTGAAGGAGAAAAGGTAGGA	5106
		TGCACATC <u>GAGAAGAG</u>	5107
		CTCTTCT <u>CAGATGTG</u> CA	5108
10	Male-sterile AG <i>Zea mays</i> Glu5Term GAA-TAA	TACCTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCG <u>AAGAGGAGG</u> CTACACCACAGTAACAG GCATCATGTCGACCCCTGACTTCGGCGGGGC	5109
		GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTGTAGCCTCCTCTT <u>ATCGGATGTG</u> CATGCTCTGTTCCATCA CACAGATTGAGGTCTGAAGGAGAAAAGGTAA	5110
		ACATCCG <u>AAGAGGAG</u>	5111
		CTCCTCTT <u>ATCGGATGT</u>	5112
15	Male-sterile AG <i>Zea mays</i> Glu6Term GAG-TAG	CTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCG <u>AAGAGGAGG</u> CTACACCACAGTAACAGGCA TCATGTCGACCCCTGACTTCGGCGGGGCAGC	5113
		GCTCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTGTAGCCTCTT <u>ATTCGGATGTG</u> CATGCTCTGTTCCATCA TCACACAGATTGAGGTCTGAAGGAGAAAAG	5114
		TCCGAG <u>AAGAGGAG</u>	5115
		AGCCTCCT <u>ATTCTCGG</u> A	5116
20	Male-sterile AG <i>Zea mays</i> Glu7Term GAG-TAG	TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGC ACATCCGAG <u>AAGAGGAGG</u> CTACACCACAGTAACAGGCA TGTCGACCCCTGACTTCGGCGGGGCAGCAGA	5117
		TCTGCTCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTGTAGCCT <u>ACTCTTCTCGGATGTG</u> CATGCTCTGTT CTATCACACAGATTGAGGTCTGAAGGAGAA	5118
		GAGAAGAG <u>AAGAGG</u> CTACA	5119
		TGTAGCCT <u>ACTCTTCTC</u>	5120
25	Male-sterile AG <i>Oryza sativa</i> Lys5Term AAG-TAG	GCTGGGTCA <u>GGATCGTCGGCGGGTGGCGGGGAGCAGC</u> GAGAAGATGGGGAGGGGG <u>TAGATCGAGATAAAGCGGGATCGAGAA</u> CACGACGA <u>ACCAGGCAGGTGACCTTCTGCAAGCGCC</u>	5121
		GGCGCTTG <u>CAGAAGGT</u> CACCTGCCGGTCGTGTTCTGATC CGCTT <u>TATCTCGATCT</u> <u>ACCCCCCTCCCCATCTTCGCTGCTCCCC</u> GCCGCCACCGCCGCCGACGATCCTGACCCAGC	5122
		GGAGGGGG <u>TAGATCGAG</u>	5123
		CTCGATCT <u>ACCCCCCTCC</u>	5124

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile AG <i>Oryza sativa</i> Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGGGGAGCAGCGAGAAGA TGGGGAGGGGGAAAGAT <u>T</u> AGATAAAGCGGATCGAGAACACGACG AACCGGCAGGTGACCTCTGCAAGCGCCGCAATG	5125
	CATTGCGGCCTTGAGAAGGTACCTGCCGGTCGTCGTGTC TCGATCCGCTTAT <u>T</u> AGATCTCCCCCTCCCCATCTCTCGCTG CTCCCCGCCGCCACCGCCGCCGACGATCCTGA	5126
	GGAAGAT <u>T</u> AGATAAAG	5127
	CTTTAT <u>T</u> AGATCTTCC	5128
10 Male-sterile AG <i>Oryza sativa</i> Lys9Term AAG-TAG	TCGTCGGCGGCGGTGGCGGGGGAGCAGCGAGAAGATGGGG AGGGGGAAAGATCGAGATA <u>T</u> AGCGGATCGAGAACACGACGAACCG GCAGGTGACCTCTGCAAGCGCCGCAATGGCCTCC	5129
	GGAGGCCATTGCGCGCTTGAGAAGGTACCTGCCGGTCGTC GTGTTCTCGATCCGCT <u>T</u> ATATCTCGATCTCCCCCTCCCCATCTTCT CGCTGCTCCCCGCCACCGCCGCCGACGA	5130
	TCGAGATA <u>T</u> AGCGGATC	5131
	GATCCGCT <u>T</u> ATATCTCGA	5132
	GCGGTGGCGGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAAG ATCGAGATAAAGCGGAT <u>T</u> AGAACACGACGAACCGGGCAGGTGAC CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	5133
15 Male-sterile AG <i>Oryza sativa</i> Glu12Term GAG-TAG	CCTCTTCAGGAGGCCATTGCGCGCTTGAGAAGGTACCTGC CGGTTCGTCGTGTT <u>T</u> AGATCCGCTTATCTCGATCTCCCCCTC CCCATCTCTCGCTGCCACCGCCGCCACCGC	5134
	AGCGGAT <u>T</u> AGAACACG	5135
	CGTGTTC <u>T</u> AGATCCGCT	5136

Table 16  
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
20 Male-sterile PI <i>Cucumis sativus</i> Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAAT AGACAAGTTACAT <u>A</u> GTCAAAGAGAAGAAATGGTATCATCAAAAAG CCAAAGAAATTACTGTTCTTGCATGCT	5137
	AGCATCGCAAAGAACAGTAATTCTTGGCTTTTGATGATACCAT TTCTCTCTT <u>G</u> ACTATGTAACCTGTCATTGCTTGAGTTCTATTG TTTTATTCTATTCCCTCTCCCC	5138

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTACATAGTCAAAGAG CTCTTTGACTATGTAAC	5139 5140
Male-sterile PI <i>Cucumis sativus</i> Ser22Term TCA-TGA	GAAGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAG ACAAGTTACATATT <u>GAAAGAGAAGAAATGGTATCATCAAAAAAGCC</u> AAAGAAATTACTGTTCTTGCATGCTCA TGAGCATCGCAAAGAACAGTAATTCTTGGCTTTTGATGATACC ATTCTTCTCTT <u>CAATATGTAAC</u> TTGTCTATTGCTTGAGTTCTAT TCTTTTATTCTATTCCCTCTC TACATATT <u>GAAAGAGAA</u> TTCTCTT <u>CAATATGTA</u>	5141 5142 5143 5144
Male-sterile PI <i>Cucumis sativus</i> Lys23Term AAG-TAG	AGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAGAC AAGTTACATATT <u>CATAGAGAAGAAATGGTATCATCAAAAAAGCCAAA</u> GAAATTACTGTTCTTGCATGCTCAAG CTTGAGCATCGCAAAGAACAGTAATTCTTGGCTTTTGATGATA CCATTCTTCTCT <u>ATGAATATGTAAC</u> TTGTCTATTGCTTGAGTTCTC TATTCTTTTATTCTATTCCCTCT CATATT <u>CATAGAGAAGA</u> TCTTCTCT <u>ATGAATATG</u>	5145 5146 5147 5148
Male-sterile PI <i>Cucumis sativus</i> Arg24Term AGA-TGA	GGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAGACAAG TTACATATT <u>CAAAGTGAAGAAATGGTATCATCAAAAAAGCCAAAGAA</u> ATTACTGTTCTTGCATGCTCAAGTT AAACTTGAGCATCGCAAAGAACAGTAATTCTTGGCTTTTGATG ATACCATTCTT <u>CACTTTGAATATGTAAC</u> TTGTCTATTGCTTGAGTT CTCTATTCTTTTATTCTATTCC ATTCAAAG <u>TGAAGAAAT</u> ATTCTT <u>CACTTTGAAT</u>	5149 5150 5151 5152
Male-sterile PI <i>Malus domestica</i> Tyr21Term TAC-TAG	GGGACGTGGGAAGGGTGAGATCAAGAGGATTGAGAACTCAAGTAA CAGGCAGGTGACCT <u>AGTCCAAGAGGAGGAATGGGATTATCAAGAA</u> GGCAAAGGAGATCACTGTTCTATGTGATGCT AGCATCACATAGAACAGTGTATCTCCTTGCCTTCTGATAATCCCA TTCCTCCTCTTGG <u>ACTAGGT</u> CACCTGCCTGTTACTTGAGTTCTCAA TCCTCTTGATCTCAACCTCCCACGTCCC GTGACCTAGTCCAAGAG CTCTTGG <u>ACTAGGT</u> CAC	5153 5154 5155 5156

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Male-sterile PI <i>Malus domestica</i> Lys23Term. AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGAACAGG CAGGTGACCTACTCCTAGAGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTCTATGTGATGCTAAAG	5157
	CTTAGCATCACATAGAACAGTGATCTCCTTGCCTTCTGATAATC CCATTCCCTCTAGGAGTAGGTACCTGCCTGTTACTTGAGTTCT CAATCCTCTGATCTAACCTCCCACG	5158
	CCTACTCCCTAGAGGAGG	5159
	CCTCCTCTAGGAGTAGG	5160
10 Male-sterile PI <i>Malus domestica</i> Lys30Term AAG-TAG	AGGATTGAGAACTCAAGAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATCTAGAAGGCAAAGGAGATCACTGTTCTATGTG ATGCTAAAGTATCTCTTATCATTATTCTA	5161
	TAGAATAAAATGATAAGAGATACTTAGCATCACATAGAACAGTGATC TCCTTGCCTCTAGATAATCCATTCCCTCTTGGAGTAGGTCA CCTGCCTGTTACTTGAGTTCTAACATCCT	5162
	GGATTATCTAGAAGGCA	5163
	TGCCTCTAGATAATCC	5164
	ATTGAGAACTCAAGAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAGTAGGCAAAGGAGATCACTGTTCTATGTGATG CTAAAGTATCTCTTATCATTATTCTAGCT	5165
15 Male-sterile PI <i>Malus domestica</i> Lys31Term AAG-TAG	AGCTAGAATAAAATGATAAGAGATACTTAGCATCACATAGAACAGT GATCTCCTTGCCTACTTGATAATCCATTCCCTCTTGGAGTAG GTCACCTGCCTGTTACTTGAGTTCTCAAT	5166
	TTATCAAGTAGGCAAAG	5167
	CTTGCCCTACTTGATAAA	5168
	CATTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAAATGTGAAGAGGAAAATTGAGATCAAAGAATTGAG AACTCAAGCAACAGGCAGGTTACTTACT	5169
20 Male-sterile globosa <i>Antirrhinum majus</i> Gly2Term GGA-TGA	AGTAAGTAACCTGCCTGTTGAGTTCTCAATTCTTTGATCTCA ATTTTCCCTCTCACATTTTTGTTTTGTTCTCTCTTGTGTTTG TTTGCAGATAACTATTGAAAAATG	5170
	AAAAAAATGTGAAGAGGA	5171
	TCCTCTTCACATTTTT	5172
	TTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAA CAAAAAAAATGGGATGAGGAAAATTGAGATCAAAGAATTGAGAAC TCAAGCAACAGGCAGGTTACTTACTCAA	5173
25 Male-sterile globosa <i>Antirrhinum majus</i> Arg3Term AGA-TGA	TTGAGTAAGTAACCTGCCTGTTGAGTTCTCAATTCTTTGATC TCAATTCTCTCACCCATTTTGTTTTGTTCTCTCTTGTGTT	5174
	TTTGCAGATAACTATTGAAAA	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	AAATGGGAT <u>GAGGAAAA</u>	5175
	TTTCCTCATCCCATT	5176
5 Male-sterile globosa <i>Antirrhinum majus</i> Gly4Term GGA-TGA	TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAA AAAAATGGGAAGAT <u>GAAAAATTGAGATCAAAGAATTGAGAACTCA</u> AGCAACAGGCAGGTTACTTACTCAAAGA TCTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTG ATCTCAATTTCATCTTCCCATTTTTGTTTTGTTTTCTCTCT GTTTTGTTGCAGATAACTATTGTA TGGGAAGAT <u>GAAAAATT</u>	5177 5178 5179
	AAATTTCA <u>TCTTCCCA</u>	5180
10 Male-sterile globosa <i>Antirrhinum majus</i> Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAA AATGGGAAGAGG <u>ATAAAATTGAGATCAAAGAATTGAGAACTCAAGC</u> AACAGGCAGGTTACTTACTCAAAGAGAA TTCTCTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTT TTGATCTCAATT <u>ATCCTCTTCCCATTTTTGTTTTGTTTTCTCT</u> CTTGTGTTGTTGCAGATAACTATT GAAGAGG <u>ATAAAATTGAG</u>	5181 5182 5183
	CTCAATT <u>ATCCTCTTC</u>	5184
15 Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GCTGAGCTTGC <u>TGCCCTGGATCTGTTGGAGTGGAGAACGC</u> AGTATGGGGCGCG <u>GCTAGATCAAGATCAAGAGGATCGAGAACTCT</u> ACCAACC <u>GGCAGGTGACCTCTCCAAGCGCC</u> GGCGCTTGAGAAGGT <u>CACCTGCCGGTTGGTAGAGTTCTCGATCC</u> TCTTGATCTGAT <u>CTAGCCCGCCCCATACTGCGTTCTCCACTCC</u> CAAACAGAT <u>CCAAGGGCAGCAAGAGCTCAGC</u> GGCGCG <u>GCTAGATCAAG</u>	5185 5186 5187
	CTTGAT <u>CTAGCCCGCC</u>	5188
20 Male-sterile PI <i>Zea mays</i> Lys7Term AAG-TAG	CTCTTGCTGCCCTGGATCTGTTGGAGTGGAGAACGCAGTATG GGGCGCG <u>GAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC</u> CGGCAGGT <u>GACCTCTCCAAGCGCCGGCCG</u> CGGCCCGGC <u>GCTTGAGAAGGT</u> CACCTGCCGG <u>TTGGTAGAGTT</u> TCGAT <u>CTCTGATCTAGATCTTGCCGCC</u> CACT <u>CCCACAGATCCAAGGGCAGCAAGAG</u> GCAAG <u>ATCTAGATCAAG</u>	5189 5190 5191
	CTTGAT <u>CTAGATCTTG</u>	5192

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACCTACCAAC CGGCAGGTGACCTCTCCAAGCGCCGGCG CGGCCCGGCCTTGGAGAAGGTACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCTGCCGGCCACTACCGTTCTC CACTCCAAACAGATCCAAGGGCAGCAAGAG	5193
		GCAAGATCTAGATCAAG	5194
		CTTGATCTAGATCTTGC	5195
			5196
		GATCTGTTGGAGTGGAGAACGGAGTATGGGGCGCGCAAGAT CAAGATCAAGAGGATCTAGAACTCTACCAACCGGAGGTGACCTT CTCCAAGCGCCGGCGACTGGTCAAGAAGG	5197
10	Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	CCTTCTTGACCAAGTCCGGCCGGCTTGGAGAAGGTACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTTGCCTGCCGC CCCATACTGCGTCTCCACTCCAAACAGATC AGAGGATCTAGAACTCT	5198
		AGAGTTCTAGATCCTCT	5199
			5200
		GCTGAGCTCTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGG AGTATGGGGCGCGCTAGATCGAGATCAAGAGGATCGAGAACCTCT ACCAACCGGCAGGTGACCTCTCCAAGCGCC	5201
		GGCGCTTGGAGAAGGTACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTCGATCTAGCCCGCCGGCCACTCCGTTCTCCACTCC CTAACAGATTCAAGGGCAGCAAGAGCTCAGC GGCGCGGCCTAGATCGAG	5202
15	Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	CTCGATCTAGCCCGCC Male-sterile PI <i>Zea mays</i> Glu7Term GAG-TAG	5203
		CTCGATCTAGCCCGCC	5204
		CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACCTACCAAC CGGCAGGTGACCTCTCCAAGCGCCGGCG CGGCCCGGCCTTGGAGAAGGTACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCTGCCGGCCACTACCGTTCTC CACTCCCTAACAGATTCAAGGGCAGCAAGAG	5205
		GCAAGATCTAGATCAAG	5206
		CTTGATCTAGATCTTGC	5207
20	Male-sterile PI <i>Zea mays</i> Glu7Term GAG-TAG	CTTGATCTAGATCTTGC	5208
		CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCG CGGCAAGATCGAGATCTAGAGGATCGAGAACCTACCAACCGGCA GGTGACCTCTCCAAGCGCCGGCGACTGG	5209
		CCAGTCCGGCCGGCTTGGAGAAGGTACCTGCCGGTTGGTA GAGTTCTCGATCCTCTAGATCTCGATCTTGCCTGCCGGCCACTC CGTTCTCCACTCCCTAACAGATTCAAGGGCAG	5210
25	Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCGAGAT <u>C</u> AGAGGATC	5211
	GATCCT <u>C</u> T <u>A</u> GATCTCGA	5212
5 Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CGAGATCAAGAGGA <u>T</u> <u>C</u> AGAACTCTACCAACC <u>G</u> GCAGGTGACCTT CTCCAAGCGCCGGCCGGACTGGTCAAGAAGG	5213
	CCTTCTTGACCAGTCCGGCCGGCGCTTGGAGAAAGGTACCTGC CGGTTGGTAGAGTT <u>T</u> <u>A</u> GATCCTCTTGATCTCGATCTGCCGC CCCATA <u>T</u> CCGTTCCACTCCCTAACAGATT	5214
	AGAGGAT <u>C</u> AGAACTCT	5215
	AGAGTT <u>T</u> <u>C</u> T <u>A</u> GATCCTCT	5216
	TTGCTGCTAAC <u>G</u> CTAG <u>T</u> GGAGGAAGGAGGAGGAGGAGGAGG CGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGA <u>T</u> <u>C</u> GAGAACT CCACCAACC <u>G</u> CCAGGTGACCTTCTCCAAGCGCA	5217
10 Male-sterile PI <i>Oryza sativa</i> Lys5Term AAG-TAG	TGCGCTTGGAGAAAGGTACCTGGCGGTGGTGGAGTTCTCGATCC TCTTGATCTCGAT <u>T</u> <u>A</u> CCC <u>G</u> CGCCCCATCCGCCTCCCTC CTCCTCCTCCAGCTAGCTAGCAGCAA	5218
	GGCGCGGG <u>T</u> <u>A</u> GATCGAG	5219
	CTCGAT <u>T</u> <u>A</u> CCCGCGCC	5220
	CTAAC <u>G</u> CTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGG TGGGGCGCGGGAAAGAT <u>T</u> <u>A</u> GATCAAGAGGA <u>T</u> <u>C</u> GAGAACTCCACC AACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG	5221
	CGCTCCTGCGCTTGGAGAAAGGTACCTGGCGGTGGTGGAGTT TCGATCCTCTTGAT <u>T</u> <u>A</u> GATCTCCCGCGCCCCATCCGCCTCC CCTCCTCCTCCCTCCAGCTAGCTAGCTAG	5222
15 Male-sterile PI <i>Oryza sativa</i> Glu7Term GAG-TAG	GGAAGAT <u>T</u> <u>A</u> GATCAAG	5223
	CTTGAT <u>T</u> <u>A</u> GATCTCC	5224
	TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGC GCGGGAAAGATCGAGAT <u>T</u> <u>A</u> GAGGATCGAGAA <u>T</u> <u>C</u> CCACCAACC <u>G</u> C CAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC	5225
	GGATCCCGCTCCTGCGCTTGGAGAAAGGTACCTGGCGGTGGT GAGTTCTCGAT <u>T</u> <u>A</u> GATCTCGATCTCCCGCGCCCCATCCCG CCTCCTCCTCCCTCCCTCCAGCTA	5226
	TCGAGAT <u>T</u> <u>A</u> GAGGATC	5227
20 Male-sterile PI <i>Oryza sativa</i> Lys9Term AAG-TAG	GATCCT <u>T</u> <u>A</u> GATCTCGA	5228

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI Oryza sativa Glu12Term GAG-TAG	GAAGGGAGGAGGAGGAGGAGGAGGGATGGGGCGCGGGAAAGA TCGAGATCAAGAGGGAT <u>CTAGA</u> ACTCCACCAACCGCCAGGTGACCT TCTCCAAGCGCAGGAGCAGGGATCCTCAAGAAGG	5229
	CCTTCTTGAGGATCCGCTCCTGCGCTTGGAGAAGGTACACCTGGC GGTTGGTGGAGTT <u>CTAGA</u> TCCCTTGATCTCGATCTTCCCGGCC CCATCCCGCCTCCTCCCTCCCTCCCTTC	5230
	AGAGGAT <u>CTAGA</u> ACTCC	5231
	GGAGTT <u>CTAGA</u> TCCCT	5232

**Example 7**  
**Engineering plants for abiotic stress tolerance**

Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The 5 worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing 10 levels of alcohol dehydrogenase can confer enhances flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which 15 results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

20 The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

**Table 17**  
**Genome-Altering Oligos Conferring Stress Tolerance**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Salt Tolerance P5CS <i>Arabidopsis thaliana</i> Phe128Ala TTT-GCT	CGTCTTTTGTGGTAGTGGATGTGACGGTGCTCAAATGCTT GTGACCGATAGCAGT <u>GCT</u> AGAGATAAGGATTCAAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	5233
		TCATCCTCAGCATCGCTTGACAGTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCT <u>AGC</u> ACTGCTATCGGTACAAGCATTGAGCAACC GTCACATCCAACCTACCACACAAAAAGACG	5234
		ATAGCAGT <u>GCT</u> AGAGAT	5235
		ATCTCT <u>AGC</u> ACTGCTAT	5236
10	Salt Tolerance P5CS 1 <i>Brassica napus</i> Phe128Ala TTC-GCC	GAGACTATGTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGT <u>GCC</u> AGAGACAAGGAGTTCAAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTGA	5237
		TCAAATCAAGCATGGACTTCACTGTCTCATTAAAGTTGCTTCCTGAA CTCCTTGTCTCT <u>GGC</u> ACTACTGTCAATTCAACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	5238
		ACAGTAGT <u>GCC</u> AGAGAC	5239
		GTCTCT <u>GGC</u> ACTACTGT	5240
		GAGACTATGTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGT <u>GTC</u> AGAGATAAGGATTCAAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTAAAATGA	5241
15	Salt Tolerance P5CS 2 <i>Brassica napus</i> Phe129Ala TTC-GCC	TCATTTCAGCATAGCTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCT <u>GAC</u> ACTGCTATCAGTCACCAGCATTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	5242
		ATAGCAGT <u>GTC</u> AGAGAT	5243
		ATCTCT <u>GAC</u> ACTGCTAT	5244
		GATATGTTGTTAACCAACTGGATGTCTCGTCATCTCAACTTCTG TCACCGACAGTGT <u>GCT</u> GAGAACCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	5245
		TAAGATCTAATAATGACTCAACAGTTCACTGAGTTGCTCCCGGAA CTTGGGTTCT <u>CAG</u> CATCACTGTGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTAAACAACATATC	5246
20	Salt Tolerance P5CS <i>Oryza sativa</i> Phe128Ala TTT-GCT	ACAGTGAT <u>GCT</u> GAGAAC	5247
		GTTCAGCATCACTGT	5248
25			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS <i>Medicago sativa</i> Phe128Ala TTT-GCT	GATATTTGTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTG TTACTGACAATGAT <u>GCTAGAGACCAAGATTTAGAAAGCAACTTC</u> TGAAACTGTGAGATCACTTCTAGCACTAA	5249
	TTAGTGCTAGAAGTGATCTCACAGTTCAAGAAAGTTGCTTCTAAA ATCTGGTCTCTAG <u>CATCATTGTCAGTAACAAGAAGCTGAGCAGAT</u> GTCACATCCAGCTGACTAAACAAATATC	5250
	ACAATGAT <u>GCTAGAGAC</u>	5251
	GTCTCTAG <u>CATCATTGT</u>	5252
Salt Tolerance P5CS <i>Actinidia deliciosa</i> Phe128Ala TTT-GCT	GATACATTGTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGAT <u>GCTAGGGATCCAGAATTAGGAAGCAACTTA</u> CTGAAACTGTAGAACATCACTATTGAATTGA	5253
	TCAAATTCAATAGTGATTCTACAGTTCAAGTTGCTTCTGAAT TCTGGATCCCTAG <u>CATCATTATCAGTAACGAGTAGCTGAGCTGAT</u> GTCACATCCAGCTGACTAAACAAATGTATC	5254
	ATAATGAT <u>GCTAGGGAT</u>	5255
	ATCCCTAG <u>CATCATTAT</u>	5256
	GACACACTCTTCAGTCACACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGAC <u>GCCAGAAGTCAGAATTAGAAAACAACCTTA</u> CTGAAACAGTCGATTCTTATTATCTTATA	5257
Salt Tolerance P5CS <i>Cichorium intybus</i> Phe122Ala TTC-GCC	TATAAGATAATAAAGAACATGACTGTTCAAGTTGTTCTAAAT TCTGGACTTCT <u>GGCGTCATTATCTGTTACAAGAAGCTGTGCTGAT</u> GTCACATCCAGTTGACTGAAGAGTGTGTC	5258
	ATAATGAC <u>GCCAGAAGT</u>	5259
	ACTTCT <u>GGCGTCATTAT</u>	5260
	GATTCTTGTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGAC <u>GCTAGAGATCCAGATTTAGGAGACAACTCAA</u> TGACACAGTAAATTGTTGCTTCTCTAA	5261
Salt Tolerance P5CS <i>Lycopersicon esculentum</i> Phe128Ala TTT-GCT	TTAGAGAAAGCAACGAATTACTGTGTCATTGAGTTGCTCCTAA ATCTGGATCTCTAG <u>CGTCATTATCAGTCACCAAGAAGCTGAGCTGA</u> TGTCACATCCAACACTGACTGAACAAAGAACATC	5262
	ATAATGAC <u>GCTAGAGAT</u>	5263
	ATCTCTAG <u>CGTCATTAT</u>	5264
	GATACCATGTTAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTG TGAATGATGGATT <u>GCTAGGGATGCTGGCTTCAGAAAACAACCTTC</u> GGACACAGTGAACCGGTTATTAGATTAA TTAAATCTAATAACCGGTTACTGTGTCGAAAGTTGTTCTGAA GCCAGCATCCCTAG <u>CAAATCCATCATTACAAGAAGTTGGGAAGA</u> AGTCACATCAAGCTGGCTGAACATGGTATC ATGGATT <u>GCTAGGGAT</u>	5265 5266 5267

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		ATCCCTAGCAAATCCAT	5268
5	Salt Tolerance P5CS <i>Mesembryanthemum crystallinum</i> Phe125Ala TTT-GCT	GACACCTTGTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGAC <u>GCT</u> AGAGATCCAAGTTAGAACACAACTA ACTGAAACAGTGTATCAGTTGGATCTAA	5269
		TTAGATCCAACAAC <u>T</u> GATAACACTGTTAGTTGTTCTAAA CTTGGATCTCT <u>AGCG</u> TCGTTGCCGTACAAGCAGCTGAGCAGCA GTCAGATCCA <u>ACTG</u> ACTAAACAAGGTGTC	5270
		ACAAACGAC <u>GCT</u> AGAGAT	5271
		ATCTCT <u>AGCG</u> TCGTTGT	5272
		GACACATTATTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGAT <u>GCT</u> AGGGATGAAGCTTCCGAAATCAACTTA CTCAAACAGTGGATTATTGTTAGCTTGA	5273
10	Salt Tolerance P5CS <i>Vitis vinifera</i> Phe130Ala TTT-GCT	TCAAAGCTAACAA <u>T</u> GAATCCACTGTTGAGTAAGTTGATTGGAA AGCTTCATCCCT <u>AGC</u> ATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC	5274
		ATAATGAT <u>GCT</u> AGGGAT	5275
		ATCCCTAG <u>CAT</u> CATTAT	5276
		GATA <u>CG</u> CTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGAT <u>GCT</u> CGAGATAAGGATTTCAGGAAGCAGCCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	5277
		TCAGCGCCAACAG <u>GCA</u> CTCACAGTCTCAGTAAGCTGCTTCTGA AATCCTATCT <u>CGAGC</u> ATCGTTCCGTACAAGAAGCTGAGCCG ATGTCACAT <u>CGAGC</u> TGAGTGAACAGCGTATC	5278
15	Salt Tolerance P5CS <i>Vigna aconitifolia</i> Phe129Ala TTT-GCT	ATAACGAT <u>GCT</u> CGAGAT	5279
		ATCTCGAG <u>CAT</u> CGTTAT	5280
		AGAGATGTTCTTAGTTCAAAGAA <u>ATCTCACCTCTCAC</u> TTCTCG TCTTCACAACAG <u>TTGTC</u> ACGTTGCAA <u>ACTGCGGATTG</u> TCCTTCCAC GAATGAGAACATGATCATCTT <u>CGCAAA</u>	5281
		TTTGCGAAAGATGATCATGTTCTCATT <u>CGTGGGG</u> ACAA <u>ATCCGCA</u> GTTTGCAA <u>ACGTGAC</u> AA <u>CTGTTG</u> GAAGACGGAGAA <u>AGTGAGAGG</u> TGAGATTCTT <u>GGAA</u> CTAAGAACATCTCT	5282
		CAACAGT <u>GT</u> CACGTT	5283
20	Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Ser207Val TCC-GTC	AAACGT <u>GAC</u> AA <u>CTGTT</u>	5284
		CGAATGAGAACATGATCATCTT <u>CGCAAA</u> <u>ACTCTGGT</u> CTCATCTG GCTCCTAATCCCT <u>CTAGT</u> ACTGATGGGAA <u>ACACTTGT</u> CCCTTGC TTCTTGTT <u>GGCT</u> CATATGGGGACTTTA	5285
		TAAAGT <u>CCCC</u> CATATGAGCAA <u>ACCAAGAAGCAAGGG</u> ACAA <u>AGTG</u> TTTCCC <u>CATCAGT</u> ACT <u>AGAGGG</u> ATTAGGAGCCAGATGAGACCAGAG TTTT <u>CGAAAG</u> ATGATCATGTT <u>CTCATT</u> CG	5286
25	Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Gln237Leu CAA-CTA		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCCCT <u>T</u> AGTACTGA	5287
	TCAGTACT <u>A</u> GAGGGATT	5288
5 Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Asn332Ser AAT-AGT	AGTCTCTAGAAGGAATGAG <u>T</u> CGTACGAGAAGTGGTGGATCGT TGTTTCAAGTGGTGAG <u>T</u> TCGCGACACACCCGGAGAAACTATAGTAG ACCTCTCTACACTTCCCCAGCTATCTTGGT	5289
10 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Ser256Val TCG-GTG	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTCT CCGGTGTGT <u>C</u> CGCG <u>A</u> CTCACCAC <u>T</u> GAACAAACGATCCAACCAAC TTCTCGTACGA <u>A</u> CTCATT <u>C</u> TTCTAGAGACT	5290
	AGTGGTGAG <u>T</u> TCGCGAC	5291
	GTCGCG <u>A</u> CTCACCAC	5292
15 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Gln286Leu CAG-CTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAATGGTGACCTTTCC GTCTTCACCACC <u>G</u> GTGG <u>T</u> GACCTTGGCAGTTGTGGTTGTCCCG ACCAATGAAAACATGATTATCTTCAGCAAA	5293
	TTTGCTGAAGATAATCATGTTTCATTGGT <u>C</u> GGGACAAACCCACA ACTGGCAAAGGT <u>C</u> ACCACGGTGGTGAAGACGGAAAAGGT <u>C</u> ACCA TTTGAGACCTTCTTCTTAGCACATCTCT	5294
	CCACCGTGG <u>T</u> GACCTT	5295
	AAAGGT <u>C</u> ACCACGGTGG	5296
20 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Asn381Ser AAC-AGC	CCAATGAAAACATGATTATCTCAGCAAAACTCTGGCCTCCTCCT GATTCTCATCC <u>C</u> CT <u>G</u> GCC <u>C</u> TTCTGGGAACATGCTGTTCCCATC GAGCCTACGTTGACGCTTGGCTCATCGG	5297
	CCGATGAGCCAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCC <u>A</u> AGAAGGG <u>C</u> AGAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTGCTGAAGATAATCATGTTTCATTGG	5298
	CATCC <u>C</u> TC <u>G</u> CC <u>C</u> TT	5299
	GAAGGG <u>C</u> CA <u>G</u> AGGGATG	5300
	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGCGCGC TGTTTCAGTGC <u>G</u> TGAG <u>C</u> AGCAGACATACCGGGAGACGGTCGTC GATCTGTC <u>C</u> ACAG <u>T</u> GT <u>C</u> CCGCCATCTTGGT	5301
	ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC GCCGGTATGTCTGCT <u>G</u> CTCACGC <u>A</u> CTGAAACAGCGCGCCACGA TTTCTCACAGGAGCTTAGTCCATTCAACGATT	5302
	GTGCGTGAG <u>C</u> AGCAGAC	5303
	GTCTGCT <u>G</u> CTCACGCAC	5304

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Salt Tolerance HKT1 <i>Oryza sativa</i> Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCAT TCTCGGTACGGTC <u>G</u> TCTCGTTGCGAATGTGGGGCTCGTGCCG ACAAATGAGAACATGGCAATCTTCTCCAAGA	5305
	TCTTGAGAAGATTGCCATGTTCTCATTTGTCGGCACGAGCCCCA CATTGCAAACGAG <u>A</u> CGACCGTGACCGAGAAATGAGAACAGTGCA ATGTTGATCCCTTCTTCTTCAGTGGAGCTT	5306
	TCACGGTC <u>G</u> TCTCGTT	5307
	AAACGAG <u>A</u> CGACCGTGAA	5308
10 Salt Tolerance HKT1 <i>Oryza sativa</i> Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCC TCCTGTTCATCGGCC <u>T</u> GATTCTGCAGGCAATACACTTACCCCTCT CTTCCTAAGGCTATTGATATGGTTCTGGG	5309
	CCCAGGAACCATATCAATAGCCTAGGAAGAGAGGGTAAAGTGTAA TTGCCTGCAAGAACAT <u>C</u> AGGCCGATGAAACAGGAGGAGGAGGCCGG GTTCTGGAGAAGATTGCCATGTTCTCATTG	5310
	CATCGGCC <u>T</u> GATTCTG	5311
	CAAGAACAT <u>C</u> AGGCCGATG	5312
	CAGCTTTGATGGACTCAGCTCTTACAGAACAGATTATCAATGCATT GTTCATGGCAGTG <u>A</u> CGCAAGGCACTCGGGGGAGAACTCCATCG ACTGCTCACTCATCGCCCCCTGCTGTTCTAGT	5313
15 Salt Tolerance HKT1 <i>Oryza sativa</i> Asn363Ser AAC-AGC	ACTAGAACAGCAGGGCGATGAGTGAGCAGTCGATGGAGTTCTC CCCCGAGTGCCTTGC <u>G</u> CTACTGCCATGAACAATGCATTGATAAT CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	5314
	GGCAGTG <u>A</u> CGCAAGGC	5315
	GCCTTGC <u>G</u> CTCACTGCC	5316
	GTGCCCACTGAACAAAGAACAGGATCAACATCGTGC <u>T</u> CTC TATCAGTCACCGTTG <u>T</u> CTCCTGTGCGAATGCAGGACTCGTGCCA CAAATGAGAACATGGTCATCTTCTCAAAGAA	5317
	TTCTTGAGAACATGACCATGTTCTCATTTGTTGGCACGAGTCCT GCATTGCCACAGGAG <u>A</u> CACACGGTGA <u>T</u> GTGAGAACAGCAC GATGTTGATCCCTTCTTGTTCAGTGGGGAC	5318
20 Salt Tolerance HKT1 <i>Triticum aestivum</i> Ala240Val GCC-GTC	CACCGTTG <u>T</u> CTCCTGTG	5319
	CACAGGAG <u>A</u> CACACGGTGA	5320
	CAAATGAGAACATGGTCATCTCTCAAAGAACATTGAGGCCCTTGT GCTGCTGAGTGGCC <u>T</u> GATGCTCGCAGGCAATACATTGTTCCCTCT CTTCCTGAGGCTACTGGTGTGGTTCTGGG	5321
	CCCAGGAACCACACCA <u>G</u> GTAGCCTCAGGAAGAGAGGGAACAAATGT ATTGCCTGCGAGC <u>A</u> GGCCACTCAGCAGCAACAAAGAGGCCCTG AATTCTTGAGAACATGACCATGTTCTCATTG	5322
	GAGTGGCC <u>T</u> GATGCTG	5323
25 Salt Tolerance HKT1 <i>Triticum aestivum</i> Gln270Leu CAG-CTG		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CGAGGCATCAGGCCACTC	5324
Salt Tolerance HKT1 <i>Triticum aestivum</i> Asn365Ser AAT-AGT	CAGTCTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT CTTCATGGTGGTGAGTGGCAGGGCACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCGCCATTATAGT	5325
	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCCTCGCACTCACCACCATGAAGAATGCATTGACAGTC TTCTGATAAGAGCTGAGCCCATCAAAGACTG	5326
	GGTGGTGAGTGCAGGGC	5327
	GCCTCGCACTCACCACC	5328
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg7Term CGA-TGA	TTTTTTTGTTCGTTTCAAAAACAAAATCTTGAATTATGGCA ACCCGTCTTCTCTGAACAAACTTATCCGGCGATCTTACCGTTAC CCGCTTTAGCCCCGTGGGTCCCTCCA	5329
	TGGGAGGACCCACCGGGCTAAAGCGGGTAAACGGTAAGATCGC CGGATAAAAGTTGTTCAAGAGAAGACGGGTTGCCATAAAATTCAA GATTTTGTTTTGAACGAAAACAAAAA	5330
	GTCTTCTCTGAACAAAC	5331
	GTTTGTTCAAGAGAAGAC	5332
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg13Term CGA-TGA	TCAAAAACAAAATCTTGAATTATGGCAACCCGTCTCTCAGAA CAAACTTTATCCGGTGAATCTTACCGTTACCCGCTTTAGCCCCGT GGGTCCCTCCCACCGTGAACGCTTACCG	5333
	CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAGC GGTAAACGGTAAGATCACCGGATAAAAGTTGTTCTGAGAAGACG GGTTGCCATAAAATTCAAAGATTTGTTTGA	5334
	TTATCCGGTGAATCTTAC	5335
	GTAAGATCACCGGATAA	5336
Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Tyr15Term TAC-TAG	AAAATCTTGAATTATGGCAACCCGTCTCTCGAACAAACTTTA TCCGGCGATCTTACCGTTACCCGCTTTAGCCCCGGTGGGTCTC CCACCGTGAACGCTTACCGGCCGTGTC	5337
	GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACGCTAAGATCGCCGGATAAAAGTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATTT	5338
	CGATCTTACCGTTACC	5339
	GGTAAACGCTAAGATCG	5340

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Leu17Term TTA-TAA	CTTGAATTATGGCAACCGTCTCCGAACAAACTTATCCG GCGATCTTACCGTAAACCCGCTTTAGCCCGGTGGGTCTCCCAC CGTACTGCTTCCACCGCCGTCGTCCCGA	5341
		TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCA CCGGGCTAAAAGCGGGTAAACGGTAAGATGCCGGATAAAGTTG TTCGGAGAAGACGGTGCATAAAATTCAAAG	5342
		TTACCGTAAACCCGCTT	5343
		AAGCGGGTAAACGGTAA	5344
10	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Gly42Term GGA-TGA	CCGGTGGGTCTCCACCGTGAUTGCTCCACCGCCGTCGTCCC GGAGATTCTCTCCCTTIGACAACAAGCACCAGAACCCCTCTCA CCACCCAAAACCCACCGAGCAATCTCACGATG	5345
		CATCGTGAGATTGCTCGGTGGGTTGGGTGGTGAAGAGGTGGT TCCGGTGCTTGTGTCAAAAGGAGAGAATCTCCGGGACGACGGC GGTGGAAAGCAGTCACGGTGGGAGGACCCACCGG	5346
		TCTCCTTIGACAACAA	5347
		TTGTTGTCAAAAGGAGA	5348
15	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Arg4Term CGA-TGA	ACATGAAGCAGTGAAATCTCTGTTGTATTGAATCTTATTAGTC AACTATGAATTCTGACAAGAGAAGTTGTAAAGTCAGTGTCCAG ATTTGTCTCATTGAATTCTAAGTCGTGA	5349
		TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTAC AAACTCTCTGTCAAGAAATTCAATGAGACTAATAAGATTCAA TACAAACAGAGATTCACTGCTTCATGT	5350
		TGAATTCTGACAAGAG	5351
		CTCTTGTCAAGAAATTCA	5352
		TGAAGCAGTGAAATCTCTGTTGTATTGAATCTTATTAGTC TATGAATTCCGATAAGAGAAGTTGTAAAGTCAGTGTCCAGATT TGTCTCATTGAATTCTAAGTCGTGAAGC	5353
20	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Gln5Term CAA-TAA	GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCT TACAAACTCTCTATCGGAAATTCAATGAGACTAATAAGATT CAATACAAACAGAGATTCACTGCTTC	5354
		ATTCCGATAAGAGAG	5355
		CTTCTCTTATCGGAAAT	5356
25	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	AGCAGTGAAATCTCTGTTGTATTGAATCTTATTAGTC GAATTCCGACAATAGAAGAGTTGTAAAGTCAGTGTCCAGATTGT CTCATTGAATTCTAAGTCGTGAAGCTTAA	5357
		TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTG CCTTACAAACTCTATTGTGGAAATTCAATGAGACTAATAAGATTAA GATTCAATACAAACAGAGATTCACTGCT	5358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACAATAGAAGTTT	5359
	AAACTTCTATTGTCGGA	5360
5 Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Lys7Term AAG-TAG	AGTGAATCTCTGTTGTATTGAATCTTATTAGTCTCAAACATATGAA TTTCCGACAAGAGTAGTTGTAAGGTCAGTGTCCAGATTGTCTC ATTGAATTCTAAGTCGTGAAGCTTAATT AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACAC TGACCTTACAAACTACTCTTGTGCGAAATTCAAGAGACTAA TAAGATTCAATACAAACAGAGATTCACT GACAAGAGTAGTTGTA	5361 5362 5363 5364
10 Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTGATTCTTCTTCACITTC TCGGATCAGGTTTAAGATTGGAAGTCGGATAAGACTTCCTCCGA CGTGAATATTCCGGTAAAACGAGATT GAATCTCGTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATC CGACTTCCAATCTTAAACCTGATCCGAGAAAGTGAAGAAGAATC GAATTAAAGCTTCACGACTTAGAATTCAATG TCAGGTTTAAGATTGG	5365 5366 5367 5368
15 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln5Term CAA-TAA	TGGAAGTCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAA GTTATGAATCACCGCTAACGACGAGTTGTGAGGTTTCAGGATTGG AAATCAGAGAGAACGCTCTGAGGGAAATTTC GAAAATTCCCTCAGAGCTCTCTGATTCCAATCCTGAAACCT CACAAACTCGTCTTAGCGGTGATTCTAAACTTAGCCAATGCATCA ACCTGCTCAACGTGGGGGATTGACTTCCA ATCACCGCTAACGACGAG	5369 5370 5371 5372
20 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gly7Term GAG-TAG	TCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG AATCACCGCCAAGACTAGTTGTGAGGTTTCAGGATTGGAAATCA GAGAGAACGCTCTGAGGGAAATTTCATGCTA TAGCATGAAAATTCCCTCAGAGCTCTCTGATTCCAATCCTG AAACCTCACAAACTAGTCTGGCGGTGATTCTAAACTTAGCCAAT GCATCAACCTGCTAACGTGGGGATTGA GCCAAGACTAGTTGTG	5373 5374 5375 5376

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC GAGTTTGTGAGGTTT <u>T</u> AGGATTGGAAATCAGAGAGAAGCTCTGAG GGAAATTTCATGCTAAAGGTGGAGTCCACC	5377
		GGTGGACTCCACCTT <u>T</u> AGCATGAAAATTCCCTCAGAGCTCTCTC TGATTTC <del>CA</del> ATC <u>T</u> AAACCTCACAAACTCGTCTGGCGGTGATT ATAACTT <del>AG</del> CCAATGCATCACCTGCTC	5378
		TGAGGTTT <u>T</u> AGGATTGG	5379
		CCAATCCT <u>AA</u> ACCTCA	5380
		TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTGT GAGGTTTCAGGATT <u>T</u> AAATCAGAGAGAAGCTCTGAGGGAAATT TCATGCTAAAGGTGGAGTCCACC <u>GA</u> AGTAA	5381
10	Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Trp14Term TGG-TGA	TTTACTTCGGTGGACTCCACCTT <u>T</u> AGCATGAAAATTCCCTCAGAG CTTCTCTGATT <u>T</u> ACAATCCTGAAACCTCACAAACTCGTCTTGGC GGTGATT <del>CATA</del> ACTT <del>AG</del> CCAATGCATCA	5382
		CAGGATT <u>T</u> AAATCAGA	5383
		TCTGATT <u>T</u> ACAATCCTG	5384
		GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTGT AGGTTTCAGGATT <u>T</u> GAATCAGAGAGAAGCTCTGAGGGAAATT CATGCTAAAGGTGGAGTCCACC <u>GA</u> AGTAAAG	5385
		CTTTACTTCGGTGGACTCCACCTT <u>T</u> AGCATGAAAATTCCCTCAGA GCTTCTCTGATT <u>T</u> ACAATCCTGAAACCTCACAAACTCGTCTTGG CGGTGATT <del>CATA</del> ACTT <del>AG</del> CCAATGCATC	5386
15	Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Lys15Term AAA-TAA	AGGATTGG <u>T</u> AAATCAGAG	5387
		CTCTGATT <u>T</u> ACAATCCT	5388
		CTTGAAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCCTGG TGGAGATAATGATG <u>T</u> AAAGAGAGGACAGATATGTTAGATT <u>C</u> AGGA CTGCAAATCAGAGCAATCTGTTATCTCAG	5389
		CTGAGATAACAGATTGCTCTGATT <u>T</u> GCAGTCCTGAAATCTAACATA TCTGTCCTCTCTT <u>T</u> ACATCATTATCTCCACCAGGCGAACAGTTAGC AGCTAAGAGTGGTAGATCAATTCTCAAG	5390
		TAATGAT <u>T</u> AAAGAGAG	5391
20	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu2Term GAA-TAA	CTCTCTT <u>T</u> ACATCATTAA	5392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTAGCTGCTAACTGTTGCCCTGGTG GAGATAATGATGGA <u>A</u> GAGAGGACAGATATGTTAGATTTCAGGAC TGCAAATCAGAGCAATCTGTTATCTCAGAGA	5393
	TCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTGAAATCTAAC ATATCTGTCCTCTC <u>A</u> TTCCATCATTATCTCCACCAGGCGAACAGTT AGCAGCTAACAGAGTGGTAGATCAATTCTTC	5394
	TGATGGA <u>A</u> TGAGAGGAC	5395
	GTCCTCTC <u>A</u> TTCCATCA	5396
10 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu4Term GAG-TAG	GAATTGATCTACCACTCTAGCTGCTAACTGTTGCCCTGGTGGAG ATAATGATGGA <u>A</u> AGATAGGACAGATATGTTAGATTTCAGGACTGCA AATCAGAGCAATCTGTTATCTCAGAGAACG	5397
	CGTTCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTGAAATCT AACATATCTGTCCT <u>A</u> CTTTCCATCATTATCTCCACCAGGCGAACACA GTTAGCAGCTAACAGAGTGGTAGATCAATT	5398
	TGGAAAG <u>A</u> TAGGACAGA	5399
	TCTGTCCT <u>A</u> CTTTCCA	5400
	ATCTACCACTCTAGCTGCTAACTGTTGCCCTGGTGGAGATAATG ATGGAAAGAGAGG <u>A</u> CT <u>G</u> ATATGTTAGATTTCAGGACTGCAAATCA GAGCAATCTGTTATCTCAGAGAACGCA <u>G</u> AGTT	5401
15 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg6Term AGA-TGA	AAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTG AAATCTAACATATC <u>A</u> GTCCCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAACAGAGTGGTAGAT	5402
	GAGAGG <u>A</u> CT <u>G</u> ATATGTT	5403
	AACATATC <u>A</u> GTCCCTCTC	5404
	CCACTCTTAGCTGCTAACTGTTGCCCTGGTGGAGATAATGATGGA AAGAGAGGACAGAT <u>A</u> GGTTAGATTTCAGGACTGCAAATCAGAGCA ATCTGTTATCTCAGAGAACGCA <u>G</u> AGTTCA	5405
	TGGTGAACACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGCAG TCCCTGAAATCTAAC <u>C</u> ATCTGTCCTCTTTCCATCATTATCTCCAC CAGGCGAACAGTTAGCAGCTAACAGAGTGG	5406
20 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Tyr7Term TAT-TAG	GACAGATA <u>GG</u> TTAGATT	5407
	AATCTAAC <u>C</u> ATCTGTC	5408
	ATCCTCTCTGAGAAAAAACACAGATCCGA <u>A</u> TTTATCTTTAATCA GCCGGAAAAATG <u>A</u> GAAGCGATCGAGAGACAACGCGTTCTTCT TGAGCATCTCCGACCTCTTCTTCTT	5409
	AAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGGCGTTGTC TCTCGATCGTTCT <u>A</u> CAATTTCGGCTGATTAAGATAAAATT GGATCTGTTGTTCTCAGAGAAGGAT	5410
25 30 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu2Term GAG-TAG		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Lys3Term AAA-TAA	AAAAAATGTAGAAAGCG	5411
	CGCTTTCT <u>A</u> CATTTTT	5412
	CTTCTCTGAGAAAAACACAGATCCGAATTATCTTAATCAGC CGGAAAAAATGGAG <u>T</u> AAGCGATCGAGAGACAACGCCGTTCTTCTG AGCATCTCCGACCTCTTCTTCTTCTCGC	5413
	GCGAAGAAGAAGAAGAAGGTGGAGATGCTCAAGAAGAACGCGT TGTCTCTGATCGCT <u>A</u> CTCCATTTTCCGGCTGATTAAAGATAA	5414
	AATTGGATCTGTTGTTTCTCAGAGAAG	
	AAATGGAG <u>T</u> AAGCGATC	5415
	GATCGCT <u>A</u> CTCCATT	5416
	GAAAAAACACAGATCCGAATTATCTTAATCAGCCGGAAAAAA TGGAGAAAGCGAT <u>C</u> TAGAGACAACGCCGTTCTTCTGAGCATCTCC GACCTTCTTCTTCTTCTCGCACAATTACG	5417
	CGTAATTGTGCGAAGAAGAAGAAGAAGGTGGAGATGCTCAAGAA GAACGCCGTTGTCT <u>C</u> AGATCGCTTCTCCATTTTCCGGCTGATT AAAGATAAAATTGGATCTGTTGTTTTC	5418
	AAGCGAT <u>C</u> TAGAGACAA	5419
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	TTGTCT <u>C</u> TAGATCGCTT	5420
	AAAACACAGATCCGAATTATCTTAATCAGCCGGAAAAATGG AGAAAGCGATCGAG <u>T</u> GACAACGCCGTTCTTCTGAGCATCTCCGAC CTTCTTCTTCTTCTCGCACAATTACGAGG	5421
	CCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTGGAGATGCTCAA GAAGAACGCCGTTGT <u>C</u> ACTCGATCGCTTCTCCATTTTCCGGCT GATTAAAGATAAAATTGGATCTGTTGTTT	5422
	CGATCGAG <u>T</u> GACAACCGC	5423
	GCGTTGT <u>C</u> ACTCGATCG	5424
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Arg7Term AGA-TGA	ACAACAGATCCGAATTATCTTAATCAGCCGGAAAAATGGAGA AAGCGATCGAGAG <u>A</u> ACGCCGTTCTTCTGAGCATCTCCGACCTT CTTCTTCTTCTCGCACAATTACGAGGCTT	5425
	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTGGAGATGCT CAAGAACGCCGTT <u>A</u> CTCTCGATCGCTTCTCCATTTTCCGG CTGATTAAAGATAAAATTGGATCTGTTGT	5426
	TCGAGAG <u>A</u> ACGCCGTT	5427
	AACGCCGTT <u>A</u> CTCTCGA	5428

Phenotype Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance glyoxysomal beta- ketoacyol-thiolase precursor <i>Brassica napus</i> Glu26Term GAA-TAA	GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCTTCTTCTT CCTCTCACAGCTT <u>I</u> AAGGCTCTCTCTGCTTCAGCTTGCTTGGC TGGGGACAGTGCTGCGTATCAGAGGACCT	5429
	AGGTCCCTTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAA GCAGAGAGAGAGCCTT <u>AAA</u> AGCTGTGAGAGGAAGAAGAAGAAGG ACGGAGATGTTCAAGAAGAACTTTGTCTCTC	5430
	ACAGCTT <u>I</u> AAGGCTCT	5431
	AGAGCCTT <u>AAA</u> AGCTGT	5432
10 2,4-DB resistance glyoxysomal beta- ketoacyol-thiolase precursor <i>Brassica napus</i> Ser32Term TCA-TGA	TTGAACATCTCCGTCTTCTTCTTCTCACAGCTTGAAGG CTCTCTCTGCTT <u>G</u> AGCTTGCTGGCTGGGACAGTGCTGCGTA TCAGAGGACCTCTCTATGGAGATGATGT	5433
	ACATCATCTCCATAGAGAGAGGTCCTTGATACGCAGCACTGTCC CCAGCCAAGCAAGCT <u>C</u> AAGCAGAGAGAGAGCCTCAAAGCTGTG AGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	5434
	CTCTGCTT <u>G</u> AGCTTGCT	5435
	AGCAAGCT <u>C</u> AAGCAGAG	5436
	TCTCCGTCTTCTTCTTCTCACAGCTTGAAGGCTCTCTC TCTGCTT <u>C</u> AGCTT <u>G</u> ATTGGCTGGGACAGTGCTGCGTATCAGAG GACCTCTCTATGGAGATGATGTAGTCATT	5437
15 20 2,4-DB resistance glyoxysomal beta- ketoacyol-thiolase precursor <i>Brassica napus</i> Cys34Term TGC-TGA	AATGACTACATCATCTCCATAGAGAGAGGTCCTTGATACGCAGC ACTGTCCCCAGCCA <u>A</u> TCAGCTGAAGCAGAGAGAGAGCCTCAA GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5438
	TCAGCTT <u>G</u> ATTGGCTGG	5439
	CCAGCCA <u>A</u> TCAGCTGA	5440
	TCCGTCTTCTTCTTCTCACAGCTTGAAGGCTCTCTC TGCTT <u>C</u> AGCTT <u>G</u> CT <u>A</u> GGCTGGGACAGTGCTGCGTATCAGAGGA CCTCTCTATGGAGATGATGTAGTCATTGT	5441
	ACAATGACTACATCATCTCCATAGAGAGAGGTCCTTGATACGCA GCACTGTCCCCAGCC <u>T</u> AGCAAGCTGAAGCAGAGAGAGAGCCTTC AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5442
25 2,4-DB resistance glyoxysomal beta- ketoacyol-thiolase precursor <i>Brassica napus</i> Leu35Term TTG-TAG	AGCTTGCT <u>A</u> GGCTGGGG	5443
	CCCCAGCCTAGCAAGCT	5444

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Tyr42Term TAT-TAG	TCACAGCTTGAAGGCTCTCTCTGCTTCAGCTTGCTGGCTGG GGACAGTGCTGCGTAG <u>CAGAGGACCTCTCTATGGAGATGATGT</u> AGTCATTGTTGCGGCACATAGGACTGCACTA	5445
	TAGTGCAGTCCTATGTGCCGACA <u>ATGACTACATCATCTCCATA</u> GAGAGAGGGCTCTGCT <u>ACGCAGCACTGTCCCCAGCCAAGCAAG</u> CTGAAGCAGAGAGAGAGCCTCAAAGCTGTGA	5446
	GCTGCGTAG <u>CAGAGGAC</u>	5447
	GTCCTCTGCTACGCAGC	5448
10 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTGCTCCAGCATCTCCGCCCTCTAATTCTT CTTCTCACAATT <u>AGGAGTCCGCTTGCCGCATCAGTATGTGCT</u> GCAGGGGATAGCGCCGCATATCATAGGGCT	5449
	AGCCCTATGATATGCGGCCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACT <u>CTAATTGTGAGAAGAAGAATTAGAAGGGC</u> GGAGATGCTGGAGCAACACTTGCTGTCTGTT	5450
	CACAATT <u>AGGAGTCCGC</u>	5451
	GCGGACT <u>CTAATTGTG</u>	5452
	2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Glu26Term GAG-TAG	5453
15 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Glu26Term GAG-TAG	AACAGACAGCAAGTGTGCTCCAGCATCTCCGCCCTCTAATTCTT CTTCTCACAATT <u>ACTAGTCCGCTTGCCGCATCAGTATGTGCT</u> CAGGGGATAGCGCCGCATATCATAGGGCT	5454
	AAGCCCTATGATATGCGGCCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACT <u>AGTAATTGTGAGAAGAAGAATTAGAAGGG</u> CGGAGATGCTGGAGCAACACTTGCTGTCTGTT	5455
	ACAATT <u>ACTAGTCCGCT</u>	5456
	AGCGGACT <u>AGTAATTGT</u>	5457
20 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Ser32Term TCA-TGA	TCCAGCATCTCCGCCCTCTAATTCTTCTCACAATTACGAGTC CGCTTTGCCGCAT <u>GAGTATGTGCTGCAGGGGATAGCGCCGCAT</u> ATCATAGGGCTTGT <u>TTATGGAGACGATGT</u>	5458
	ACATCGTCTCCATAAAACAGAAGCCCTATGATATGCGGCCTATCC CCTGCAGCACATACT <u>CATGCGGCAAGAGCGGACTCGTAATTGTGA</u> GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	5459
	TGCCGCAT <u>GAGTATGTG</u>	5460
	CACATACT <u>CATGCGGCA</u>	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Cys34Term TGT-TGA	TCTCCGCCCTCTAATTCTTCTCACATTACGAGTCGCTCTT GCCGCATCAGTATGAGCTGCAGGGGATAGCGCCGATATCATAG GGCTTCTGTTATGGAGACGATGTGGTGATT	5461
	AATCACACATCGTCTCCATAAACAGAACGCTATGATATGCGGC GCTATCCCCTGCAGC <u>I</u> CATACTGATGCGGCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	5462
	TCAGTATG <u>G</u> CTGCAGG	5463
	CCTGCAGC <u>I</u> CATACTGA	5464
10 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr42Term TAT-TAG	TCACAATTACGAGTCGCTTGCAGCATCAGTATGTGCTGCAGG GGATAGCGCCGCAT <u>A</u> GCATAGGGCTCTGTTATGGAGACGATGT GGTGATTGTCAGCTCATCGTACTGCACCT	5465
	AAGTGCAGTACGATGAGCTGCCAACATCACACATCGTCTCCATA AACAGAACGCTATG <u>C</u> TATGCGGCCTATCCCCTGCAGCACATAC TGATGCGGCAAGAGCGGACTCGTAATTGTGA	5466
	GCCGCAT <u>A</u> GCATAGGGC	5467
	GCCCTATG <u>C</u> TATGCGGC	5468
	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Tyr22Term TAC-TAG	5469
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Tyr22Term TAC-TAG	GAAGGGCGATCAACAGGCAGAGCATTGCTACATCATCTCCGGCC TTCTTCTTCCGCTT <u>A</u> CAAAATGAATCTCGCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCTTCGTATCAA	5469
	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCGAGAGAG CGAAGATTCAATTG <u>T</u> CAAGCGGAAGAAGAAGGCCGGAGATGATG TAGCAAAATGCTCTGCCTGTTGATGCCCTC	5470
	TCCGCTT <u>A</u> CAAAATGA	5471
	TCATTG <u>T</u> CAAGCGGA	5472
	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Glu25Term GAA-TAA	5473
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTGCTACATCATCTCCGGCCTTCTT CCGCTTACACAA <u>A</u> ATCTCGCTCTGCATCGGTTGTGCAGC GGGGATAGTGCTTCGTATCAAAGGACAT	5473
	ATGTCCTTGTACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATT <u>A</u> ATTGTGAAGCGGAAGAAGAAGGCCGG AGATGATGTAGCAAAATGCTCTGCCTGTTGAT	5474
	ACACAA <u>A</u> ATCTCG	5475
	CGAAGATT <u>A</u> ATTGTG	5476

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser27Term TCG-TAG	GGCAGAGCATTGCTACATCATCTCCGGCCTTCTTCTCGCTTA CACAAATGAATCTT <u>AG</u> CTCTGCATCGGTTGTGCAGCTGGGA TAGTGCTTCGTATCAAAGGACATCGGTGTT	5477
	AACACCGATGTCCCTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAG <u>CTA</u> AGATTCAATTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAATGCTCTGCC	5478
	TGAATCTT <u>AG</u> CTCTCTG	5479
	CAGAGAG <u>CTA</u> AGATTCA	5480
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTTCTCGCTTACACAAATGAATC TTCGCTCTCTGCAT <u>AG</u> GTGTTGTGCAGCTGGGATAGTGCTTCGTA TCAAAGGACATCGGTGTTGGAGATGATGT	5481
	ACATCATCTCCAAACACCGATGTCCCTTGATACGAAGCACTATCCC CAGCTGCACAAAC <u>CTA</u> GCAGAGAGCGAAGATTCAATTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA	5482
	CTCTGCAT <u>AG</u> GTGTTGTG	5483
	CACAAAC <u>CTA</u> GCAGAG	5484
	TCATCTCCGGCCTTCTTCTCGCTTACACAAATGAATCTCGCTC TCTGCATCGGTT <u>G</u> AGCAGCTGGGATAGTGCTTCGTATCAAAGG ACATCGGTGTTGGAGATGATGTGCGTGT	5485
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Cys33Term TGT-TGA	AATCACGACATCATCTCCAAACACCGATGTCCCTTGATACGAAGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCAATT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	5486
	TCGGTTT <u>G</u> AGCAGCTGG	5487
	CCAGCTGCTCAAACCGA	5488
	GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTCGGCTT <u>AG</u> AGCCATGAATCTCGCTCTGCATCGGTT TGTGCAGCTGGGATAGTGCCTCGTATCAA	5489
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Tyr22Term TAT-TAG	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCA <u>GG</u> CTAAAGCCGAAGATGAAGGCCGGAGATGAT GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	5490
	TCGGCTT <u>AG</u> AGCCATGA	5491
	TCATGGCT <u>CTA</u> AGCCGA	5492

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT CGGCTTATAGCCATTAAATCTTCGCTCTGCATCGGTTGTGCAG CTGGGGATAGTGCCTCGTATCAAAGAACGT	5493
	ACGTTCTTGTATACGACGCACATATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATGGCTATAAGCCGAAGATGAAGGCCGG AGATGATGTAGCAGAATGCTCTGCCTGTTGAT	5494
	ATAGCCATTAAATCTTCG	5495
	CGAAGATTAAATGGCTAT	5496
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTCGGCTT ATAGCCATGAATCTTAAAGCTCTGCATCGGTTGTGCAGCTGGGG ATAGTGCCTCGTATCAAAGAACGTGGTGT	5497
	AACACCGACGTTCTTGTATACGACGCACATATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAAGATTATGGCTATAAGCCGAAGATGAA GGCCGGAGATGATGTAGCAGAATGCTCTGCC	5498
	TGAATCTTAAAGCTCTCG	5499
	CAGAGAGCTAAAGATTCA	5500
	TGCTACATCATCTCCGGCCTTCATCTCGGCTTATAGCCATGAATC TTCGCTCTGCATAGGTTGTGCAGCTGGGGATAGTGCCTCGTA TCAAAGAACGTGGTGTGGAGATGATGT	5501
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Ser31Term TCG-TAG	ACATCATCTCCAAACACCGACGTTCTTGTATACGACGCACATATCCC CAGCTGCACAAACCTAAAGCTGGAGAGCGAAGATTATGGCTATAAG CCGAAGATGAAGGCCGGAGATGATGTAGCA	5502
	CTCTGCATAGGTTGTG	5503
	CACAAACCTAAAGCAGAG	5504
	TCATCTCCGGCCTTCATCTCGGCTTATAGCCATGAATCTCGCTC TCTGCATCGGTTGAGCAGCTGGGGATAGTGCCTCGTATCAAAGA ACGTCGGTGTGGAGATGATGTGATA	5505
	TATCACGACATCATCTCCAAACACCGACGTTCTTGTATACGACGCA CTATCCCCAGCTGCCTAAACCGATGCAGAGAGCGAAGATTATGG CTATAAGCCGAAGATGAAGGCCGGAGATGA	5506
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Cys33Term TGT-TGA	TCGGTTGAGCAGCTGG	5507
	CCAGCTGCCTAAACCGA	5508
	TCATAGCTCTTGGATTCTTCCAAGGTTAGTGAGCTG CTATGGCAACTCATAGCAAACGCAACCTCCTCCGATTTCCCG CTCTTGCCGATGAAAATTCCCAGATTCAG	5509
	CTGGAATCTGGGATTTCATCGGCAAGAGCGGGAAAATCGGAAG GAGGTGCGTTGCTAAATGAGTTGCCATAGCAGCTCACTAACCTT GGAAGAACCCAAGCGGAAAAGAGACTATGA	5510

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAACTCAT <u>T</u> AGCAAACG	5511
	CGTTTGCT <u>A</u> ATGAGTTG	5512
5 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln6Term CAA-TAA	TAGTCTCTTTGCCGCTGGATTCTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAG <u>T</u> AAACGCAACCTCCCTCCGATTTCCCGCTC TTGCCGATGAAAATTCCCAGATTCCAGGTT AACCTGGAATCTGGGAATTTCATCGGCAAGAGCAGGGAAAATCGG AAGGAGGTTGCGTT <u>A</u> CTGATGAGTTGCCATAGCAGCTCACTAAC CTTGGAAAGAATCCAAGCAGGGAAAAGAGACTA CTCATCAG <u>T</u> AAACGCAA TTGCGTT <u>A</u> CTGATGAG	5513 5514 5515 5516
10 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	CTTTGCCGCTTGATTCTCCAAGGTTAGTGAGCTGCTATGGCA ACTCATCAGCAAACG <u>T</u> AACCTCCCTCCGATTTCCCGCTCTGCC GATGAAAATTCCCAGATTCCAGGTTCAATT AAATTGAAACCTGGAATCTGGGAATTTCATCGGCAAGAGCAGGGAA AATCGGAAGGAGGTT <u>A</u> CGTTGCTGATGAGTTGCCATAGCAGCTC ACTAACCTGGAAAGAATCCAAGCAGGGAAAAG AGCAAACG <u>T</u> AACCTCCT AGGAGGTT <u>A</u> CGTTGCT	5517 5518 5519 5520
15 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAGCAAACGCAACCTCCCTCCGATTT CCCGCTCTGCCGATT <u>AAA</u> ATTCCCAGATTCCAGGTTCAATTACA CCTTCTAATCATTATTCTTAATTTCCTT AAGAAAAATTAAAGAAATAATGATTAGAAGGTGTAATTGAACCTGG AATCTGGGAATT <u>T</u> AAATCGGCAAGAGCAGGGAAAATCGGAAGGAG GTTGCGTTGCTGATGAGTTGCCATAGCAGC TTGCCGATT <u>AAA</u> ATTCC GGAATT <u>T</u> AAATCGGCAA	5521 5522 5523 5524
20 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln22Term CAG-TAG	GCAACTCATCAGCAAACGCAACCTCCCTCCGATTTCCCGCTCTT GCCGATGAAAATT <u>C</u> TAGATTCCAGGTTCAATTACACCTCTAAT CATTATTCTTAATT <u>T</u> CTTGGTGGATT AATCCACCAAAGAAAAATTAAAGAAATAATGATTAGAAGGTGTAATT GAACCTGGAAT <u>T</u> AGGAATTTCATCGGCAAGAGCAGGGAAAATCG GAAGGAGGTTGCGTTGCTGATGAGTTGC AAAATT <u>C</u> TAGATTCCA TGGAAAT <u>T</u> AGGAATT <u>T</u>	5525 5526 5527 5528

**Example 8****Production of albino mutants for the analysis of photosynthetic processes**

Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

**Table 18**  
**Oligonucleotides to produce albino plants**

5 Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
10 White leaves Immutans <i>Arabidopsis thaliana</i> Ser5Term TCA-TGA	TTCTTTCCCTGTGAAATTATCTGCTCAAATCTTGGTTCCTGACGGAG ATGGCGGCGATT <u>T</u> GAGGCATCTCCTCTGGTACGTTGACGATTCA CGGCCTTGGTTACTCTCGACGCTCTAG	5529
	CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGCCT <u>C</u> AAATGCCGCCATCTCCGTAGGAACCAA AGATTGAGCAGATAATTACAGGAAAGAA	5530
	<u>G</u> GCAGATT <u>T</u> GAGGCATCT	5531
	AGATGCCT <u>C</u> AAATCGCC	5532
	GCTCAAATCTTGGTTCCTGACGGAGATGGCGGCGATT <u>T</u> CAGGCA TCTCCTCTGGTACGT <u>A</u> GACGATTACGGCCTTGGTTACTCTTCG ACGCTCTAGAGCCGCCGTTCGTACAGCTC GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAA GGCCGTGAAATCGCT <u>A</u> CGTACGTACCGAGAGGAGATGCCTGAAATGCC GCCATCTCCGTAGGAACCAAAGATTGAGC TGGTACGT <u>A</u> GACGATT	5533 5534 5535 5536
15 White leaves Immutans <i>Arabidopsis thaliana</i> Leu12Term TTG-TAG	TTGGTTCCGTACGGAGATGGCGGCGATT <u>T</u> CAGGCATCTCCTCTG GTACGTTGACGATT <u>T</u> GACGGCCTTGGTTACTCTCGACGCTCTAG AGCCGCCGTTCGTACAGCTCCTCTCACCG	5537
	CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAG AGTAACCAAAGGCCGT <u>C</u> AAATCGTCAACGTACCGAGAGGAGATGCC TGAAATGCCGCCATCTCCGTAGGAACCAA GACGATT <u>T</u> GACGGCCTT	5538 5539
	AAGGCCGT <u>C</u> AAATCGTC	5540
	GCGGCGATT <u>T</u> CAGGCATCTCCTCTGGTACGTTGACGATT <u>T</u> CACGG CCTTGGTTACTCTT <u>T</u> GACGCTCTAGAGCCGCCGTTCGTACAGCT CCTCTACCGATTGCTTACATCTTCCTC	5541
	GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG GCGGCTCTAGAGCGTC <u>A</u> AGAGTAACCAAAGGCCGTGAAATCGTC AACGTACCGAGAGGAGATGCCTGAAATGCCCGC	5542
20 White leaves Immutans <i>Arabidopsis thaliana</i> Arg22Term CGA-TGA	TTACTCTT <u>T</u> GACGCTCT	5543
	AGAGCGTC <u>A</u> AGAGTAA	5544

5	White leaves Immutans <i>Arabidopsis thaliana</i> Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTCACGGCCCTGGTTA CTCTTCGACGCTCTTGAGCCGCCGTTCTGACAGCTCCTCTCACC GATTGCTTCATCATCTCCTCTCTCTC	5545
		GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG TACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCG TGAAATCGTCAACGTACCAAGAGGAGATGCCTGA	5546
		GACGCTCTTGAGCCGCC	5547
		GGCGGCTCAAGAGCGTC	5548
		GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTCGATT CTGCTATGAGTTTGAACCTCAGTTCTCATATTCTGTAGA GCTAGGAGTTTGAGAAGTCATCAGTT	5549
10	White leaves Immutans <i>Lycopersicon esculentum</i> Gly11Term GGA-TGA	AAACTGATGACTCTCAAAACTCCTAGCTCTAAAACAAGAATATGAA GAAACTGAGGTTCAAAACTCATAGCAGAAATCGAAATGCCATTC TTGATCCTCTCCCTCCCACAAGAAC	5550
		TGAGTTTGAACCTCA	5551
		TGAGGTTCAAAACTCA	5552
		GTGGGAAGGAAGAAGGATCAAGAATGGCGATTCGATTCTGCTA TGAGTTTGGAACCTGAGTTCTCATATTCTGTAGAGCTAGG AGTTTGAGAAGTCATCAGTTATGCAA	5553
15	White leaves Immutans <i>Lycopersicon esculentum</i> Ser13Term TCA-TGA	TTGCATAAAACTGATGACTCTCAAAACTCCTAGCTCTAAAACAAGA ATATGAAGAAACTCAGGTTCCAAAACTCATAGCAGAAATCGAAATC GCCATTCTGATCCTCTCCCTCCCAC	5554
		TGGAACCTGAGTTCTT	5555
		AAGAAACTCAGGTTCCA	5556
		AAGAAGGATCAAGAATGGCGATTCGATTCTGCTATGAGTTTGG AACCTCAGTTCTTGATATTCTGTAGAGCTAGGAGTTTGAGA AGTCATCAGTTATGCAATTCCCAGAA	5557
		TTCTGGGAATTGCATAAAACTGATGACTCTCAAAACTCCTAGCTC TAAAACAAGAATATCAAGAAACTGAGGTTCCAAAACTCATAGCAGA AATCGAAATGCCATTCTGATCCTCTT	5558
20	White leaves Immutans <i>Lycopersicon esculentum</i> Ser16Term TCA-TGA	AGTTTCTTGATATTCTT	5559
		AAGAAATATCAAGAACT	5560
		AGGATCAAGAATGGCGATTCGATTCGCTATGAGTTTGGAAC TCAGTTCTTCATAGTCTTGTTAGAGCTAGGAGTTTGAGAAGTC ATCAGTTTATGCAATTCCCAGAACCCA	5561
		TGGGTTCTGGGAATTGCATAAAACTGATGACTCTCAAAACTCCTA GCTCTAAAACAAGACTATGAAGAAACTGAGGTTCCAAAACTCATAG CAGAAATCGAAATGCCATTCTGATCCT	5562
		TCTTCATAGTCTTGTT	5563
25	White leaves Immutans <i>Lycopersicon esculentum</i> Tyr17Term TAT-TAG	AAACAAGACTATGAAGA	5564

5	White leaves Immutans <i>Lycopersicon esculentum</i> Cys19Term TGT-TGA	AAGAATGGCGATTCGATTTCTGCTATGAGTTTGGAACCTCAGTT TCTTCATATTCTT <u>G</u> ATTAGAGCTAGGAGTTTGAGAACATCAGT TTTATGCAATTCCCAGAACCCATGTCGG	5565
		CCGACATGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAA CTCCTAGCTCTAA <u>A</u> CAAGAATATGAAGAAACTGAGGTTCCAAAAC TCATAGCAGAAATCGAAATGCCATTCTT	5566
		TATTCTT <u>G</u> ATTAGAGC	5567
		GCTCTAA <u>A</u> CAAGAATA	5568
		CGCGTCGATAAAAAAAATCAAGAATGGCGATTCATATCTGCTAT GAGTTT <u>C</u> GA <u>A</u> CTT <u>G</u> AGTTCTCTCATATT <u>C</u> AGCATT <u>T</u> GTGCA ATTCCAAAGAACCCATT <u>T</u> GT <u>T</u> GAATT <u>C</u>	5569
10	White leaves Immutans <i>Capsicum annuum</i> Ser13Term TCA-TGA	GAATTCAAAACAAATGGGTTCTGGATTGCACAAAATGCTGAAT ATGAAGAAGAA <u>A</u> CT <u>C</u> AA <u>G</u> TT <u>C</u> GAAA <u>A</u> CT <u>C</u> AT <u>G</u> CAGATATGGAAAT CGCCATTCTGATT <u>T</u> ATCGGACCG	5570
		TCGA <u>A</u> CTT <u>G</u> AGTTCTT	5571
		AAGAA <u>A</u> CT <u>C</u> AA <u>G</u> TT <u>C</u> G	5572
		AAAAATCAAGAATGGCGATTCATATCTGCTATGAGTTT <u>C</u> GA <u>A</u> CT TCAGTTCTT <u>C</u> TT <u>G</u> ATATT <u>C</u> AGCATT <u>T</u> GTGCAATT <u>CC</u> AA <u>GA</u> ACCC AT <u>T</u> TT <u>G</u> TT <u>G</u> ATT <u>C</u> TC <u>T</u> ATT <u>T</u> CA <u>T</u>	5573
		AGT <u>G</u> AAAATAGAGAATT <u>C</u> AA <u>AC</u> AAATGGGTTCTGGATTGCACA AAAAT <u>G</u> CT <u>G</u> AA <u>A</u> TT <u>C</u> AA <u>GA</u> AGAA <u>A</u> CT <u>G</u> AA <u>G</u> TT <u>C</u> GAAA <u>A</u> CT <u>C</u> AT <u>G</u> C AGATAT <u>G</u> AA <u>A</u> TC <u>G</u> CCATT <u>T</u> GT <u>T</u> TTT	5574
15	White leaves Immutans <i>Capsicum annuum</i> Ser17Term TCA-TGA	TT <u>C</u> TT <u>C</u> TT <u>G</u> ATATT <u>C</u> AG	5575
		CTGA <u>A</u> AT <u>T</u> <u>C</u> AA <u>GA</u> AGAA	5576
		CAAGAATGGCGATTCATATCTGCTATGAGTTT <u>C</u> GA <u>A</u> CT <u>C</u> AGT TT <u>C</u> TT <u>C</u> TT <u>G</u> ATATT <u>G</u> AG <u>C</u> ATT <u>T</u> GTGCAATT <u>CC</u> AA <u>GA</u> ACCCATT <u>T</u> GTT <u>G</u> AA <u>T</u> TC <u>T</u> CT <u>T</u> ATT <u>T</u> CA <u>T</u> TT <u>C</u> ACT <u>T</u> AG <u>G</u> AA	5577
		TT <u>C</u> CT <u>A</u> AG <u>T</u> GA <u>A</u> AA <u>A</u> TT <u>C</u> AA <u>AC</u> AAATGGGTTCTGGATT GCACAAAAT <u>G</u> CT <u>C</u> AA <u>A</u> TT <u>G</u> AA <u>GA</u> AGAA <u>A</u> CT <u>G</u> AA <u>G</u> TT <u>C</u> GAAA <u>A</u> CT <u>C</u> AT <u>G</u> AG <u>C</u> AG <u>A</u> TT <u>G</u> AA <u>A</u> TC <u>G</u> CCATT <u>T</u> GT	5578
		TT <u>C</u> AT <u>T</u> ATT <u>G</u> AG <u>C</u> ATT <u>T</u>	5579
20	White leaves Immutans <i>Capsicum annuum</i> Ser19Term TCA-TGA	AAAAT <u>G</u> CT <u>C</u> AA <u>A</u> TT <u>G</u> AA	5580
		CGATTT <u>C</u> AT <u>T</u> CTGCTATGAGTTT <u>C</u> GA <u>A</u> CT <u>C</u> AGTT <u>C</u> TT <u>C</u> CA TATT <u>C</u> AG <u>C</u> ATT <u>T</u> <u>T</u> <u>T</u> <u>G</u> CAATT <u>CC</u> AA <u>GA</u> ACCCATT <u>T</u> T <u>C</u> T <u>T</u> TT <u>C</u> ACT <u>T</u> AG <u>G</u> AA <u>T</u> CT <u>C</u> AT <u>G</u>	5581
		CTAT <u>G</u> AG <u>A</u> ATT <u>C</u> TA <u>A</u> GT <u>G</u> AA <u>A</u> TT <u>G</u> AG <u>A</u> ATT <u>C</u> AA <u>AC</u> AAATGGGTT CTT <u>G</u> GA <u>T</u> TC <u>G</u> ACT <u>A</u> AA <u>A</u> TT <u>G</u> CT <u>G</u> AA <u>A</u> TT <u>G</u> AA <u>G</u> AA <u>A</u> CT <u>G</u> AA <u>G</u> TT CGAAA <u>A</u> CT <u>C</u> AT <u>G</u> AG <u>A</u> TT <u>G</u> AA <u>A</u> TC <u>G</u>	5582
		AG <u>C</u> ATT <u>T</u> <u>T</u> <u>T</u> <u>G</u> CA <u>A</u> TT	5583
		AATT <u>G</u> CA <u>T</u> <u>A</u> AA <u>A</u> GT <u>G</u> CT	5584
25	White leaves Immutans <i>Capsicum annuum</i> Leu21Term TTG-TAG		

5	White leaves Immutans <i>Capsicum annuum</i> Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTCGAACCTCAGTTCTTCTTCATATT CAGCATTGGTGAATTCCAAGAACCCATTGGTTGAATTCTCTA TTTCACTTAGGAATTCTCATAGAAC AGTTCTATGAGAATTCTAAGTAAAATAGAGAATTCAAACAAAATG GGTTCTTGGATTACACAAAAATGCTGAATATGAAGAAGAAACTGA AGTCGAAAACATAGCAGATATGGAA TTTTGTGAATTCCAA	5585 5586 5587 5588
	White leaves Immutans <i>Oryza sativa</i> Glu22Term GAG-TAG	TTCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTGAGG AGTCCTTCCCCTCAGGTAGACGGCTCCTGACGAGCCACTGG TCACCGCCGAGGGAGCTGGTGGTAAGCTCG CGAGCTTAACCACCCAGCTCTCCTCGCGGTGACCAGTGGCTCG TCAGGAGGAGCCGTCTACCTGAAGGGGAAGGACTCCTGACGGC CACCTCGGTCTGCTCCTCTCCCTCGTGCCGAA CCTTCAGGTAGACGGCT	5589 5590 5591 5592
	White leaves Immutans <i>Oryza sativa</i> Glu28Term CAG-TAG	GAGCAGACCGAGGTGGCCGTGAGGAGTCCTTCCCCTCAGGG GACGGCTCCTCCTGACTAGCCACTGGTACCGCCGAGGAGAGCT GGGTGGTTAACGCTCGAGCAGTCCGTGAACATT AAATGTTACGGACTGCTCGAGCTAACCAACCCAGCTCCTCGG CGGTGACCAAGTGGCTAGTCAGGAGGAGCCGTCCCTGAAGGG AAGGACTCCTCGACGGCACCTCGGTCTGCTC CTCCTGACTAGCCACTG	5593 5594 5595 5596
	White leaves Immutans <i>Oryza sativa</i> Glu34Term GAG-TAG	GTCGAGGAGTCCTTCCCCTCAGGGAGACGGCTCCTGACGA GCCACTGGTCACCGCCTAGGAGAGCTGGTGGTTAACGCTCGAGC AGTCCGTGAACATTTCCTCACGGAGTCAGTCA TGACTGACTCCGTGAGGAAATGTTACGGACTGCTCGAGCTAA CCACCCAGCTCCTAGGCGGTGACCAGTGGCTCGTCAGGAGGA GCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC TCACCGCCTAGGAGAGC	5597 5598 5599 5600
	White leaves Immutans <i>Oryza sativa</i> Glu35Term GAG-TAG	GAGGAGTCCTTCCCCTCAGGGAGACGGCTCCTGACGAGCC ACTGGTCACCGCCGAGTAGAGCTGGTGGTTAACGCTCGAGCAGT CCGTGAACATTTCCTCACGGAGTCAGTCATCA TGATGACTGACTCCGTGAGGAAATGTTACGGACTGCTCGAGCT TAACCACCCAGCTCTAGTCGGCGGTGACCAGTGGCTCGTCAGGA GGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC CCGCCGAGTAGAGCTGG	5601 5602 5603 5604
10			
15			
20			
25			

5	White leaves Immutans <i>Oryza sativa</i> Trp37Term TGG-TGA	CTTCCCCTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCAC CGCCGAGGGAGAGCT <u>GAGTGGTTAAGCTCGAGCAGTCGTGAACA</u> TTTCCTCACGGAGTCAGTCATCACGATACTT	5605
		AAGTATCGTGTGACTGACTCCGTGAGGAAAATGTTCACGGACTG CTCGAGCTAACCACT <u>CAGCTCTCCTCGGCGGTGACCAGTGGCTC</u> GTCAGGAGGGAGCCGTCTCCCTGAAGGGGAAG	5606
		GAGAGCT <u>GAGTGGTTAA</u>	5607
		TTAACCACT <u>CAGCTCTC</u>	5608
		TCGGGAGGGAGGAAGGGGGATTGACGAGGGAGCTCACCCCTGCCG GCGAGGACGGCGACT <u>GAGTCGTCACTTCAGCAGTCAGTCCTTCAAC</u> GTATTCCCTCACGGATACTGTCACTTTATACTC	5609
10	White leaves Immutans <i>Triticum aestivum</i> Trp22Term TGG-TGA	GAGTATAAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTG CTCGAATCTGACGACT <u>CAGTCGCCGTCCCTGCCGGCGAGGGTGA</u> GCTCCTCGTCGAATCCCCCTCCTCCCTCGGA	5610
		GGCGACT <u>GAGTCGTCA</u>	5611
		CTGACGACT <u>CAGTCGCC</u>	5612
		GAGGAAGGGGGATTGACCGAGGGAGCTCACCCCTGCCGGCGAGG ACGGCGACTGGGTCGT <u>CTGATTGAGCAGTCCTTCAACGTATTCC</u> TCACGGATACTGTCACTTTATACTCGATATTTC	5613
		GAATATCGAGTATAAAAGATGACAGTATCCGTGAGGAATACGTTGAA GGACTGCTCGAAT <u>CAGACGACCCAGTCGCCGTCCCTGCCGGCGA</u> GGGTGAGCTCCTCGTCGAATCCCCCTCCTC	5614
15	White leaves Immutans <i>Triticum aestivum</i> Arg25Term AGA-TGA	GGGTGCT <u>CTGATTGAG</u>	5615
		CTCGAAT <u>CAGACGACCC</u>	5616
		GGGGGATTGACCGAGGGAGCTCACCCCTGCCGGCGAGGACGGCG ACTGGGTCGT <u>CAGATTCTAGCAGTCCTTCAACGTATTCC</u> TACGTCACTTTATACTCGATATTCTGTATC	5617
		GATACAGAAATATCGAGTATAAAAGATGACAGTATCCGTGAGGAATAC GTTGAAGGACTGCT <u>AGAATCTGACGACCCAGTCGCCGTCC</u> GGCGAGGGTGAGCTCCTCGTCGAATCCCC	5618
		TCAGATT <u>CTAGCAGTCC</u>	5619
20	White leaves Immutans <i>Triticum aestivum</i> Glu27Term GAG-TAG	GGACTGCT <u>AGAATCTGA</u>	5620
		GGATTCGACGAGGGAGCTCACCCCTGCCGGCGAGGACGGCGACTG GGTCGT <u>CAGATTGAGTAGTCCTTCAACGTATTCC</u> TCACTTTATACTCGATATTCTGTATCGT	5621
		CACGATA <u>CAGAAATATCGAGTATAAAAGATGACAGTATCCGTGAGGAA</u> TACGTTGAAGGACT <u>ACTCGAATCTGACGACCCAGTCGCCGTCC</u> GCCGGCGAGGGTGAGCTCCTCGTCGAATCC	5622
		GATT <u>CGAGTAGTCCTC</u>	5623
		GAAGGACT <u>ACTCGAATC</u>	5624
25	White leaves Immutans <i>Triticum aestivum</i> Gln28Term CAG-TAG		

5

White leaves	CGAGCAGTCCTCAACGTATCCTCACGGATACTGTCATCTTATA	5625
Immutans	CTCGATATTCTGT <u>AGCGT</u> GACCGCGACTACGCAAGGTTCTCGTG	
<i>Triticum aestivum</i>	CTCGAGACCATGCCAGGGTGCCCTATTTC	
Tyr46Term	GAAATAGGGCACCCCTGGCGATGGTCTCGAGCACGAAGAACCTTG	5626
TAT-TAG	CGTAGTCGCGGT <u>CACG</u> <u>CT</u> ACAGAATATCGAGTATAAAGATGACAG	
	TATCCGTGAGGAATA <u>CGTT</u> GAAGGACTGCTCG	
	ATTCTGT <u>AGCGT</u> GACCG	5627
	CGGTCACG <u>CT</u> ACAGAAT	5628

**Example 9****Altering amino acid content of plants**

Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, 5 tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

10 Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are 15 associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

20 An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

**Table 19**  
**Genome-Altering Oligos Conferring Amino Acid Overproduction**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Met Overproduction CGS <i>Arabidopsis thaliana</i> Arg77His CGT-CAT	TATCCTCCAGGATCTTAAGATTCCTCCTAATTCGTCCGTAGCT GAGCATTAAAGCCC <u>A</u> TAGAAACTGTAGCAACATCGGTGTTGCACA GATCGTGGCGGCTAAGTGGTCCAACAAACCC	5629
		GGGTTGTTGGACCACCTAGCCGCCACGATCTGTGCAACACCGAT GTTGCTACAGTTCTATGGGCTTTAATGCTCAGCTGACGGACGAA	5630
		ATTAGGAGGAAATCTTAAGATCCTGGAGGATA	
		TAAAGCCC <u>A</u> TAGAAACT	5631
		AGTTTCTATGGGCTTTA	5632
10	Met Overproduction CGS <i>Arabidopsis thaliana</i> Ser81Asn AGC-AAC	TCTTAAGATTTCTCCTAATTCGTCCGTAGCTGAGCATTAAAGC CCGTAGAAACTGT <u>A</u> CAACATCGGTGTTGCACAGATCGTGGCGG CTAAGTGGTCCAACAAACCCATCCTCCCGCGTT	5633
		AACGCGGAGGATGGGTTGTTGGACCACCTAGCCGCCACGATCTG TGCAACACCGATGTTG <u>T</u> ACAGTTCTACGGGCTTTAATGCTCAGC	5634
		TGACGGACGAAATTAGGAGGAAATCTTAAGA	
		AAACTGTA <u>A</u> CAACATCG	5635
		CGATGTTG <u>T</u> ACAGTT	5636
15	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Ser GGT-AGT	TTCCCTCCTAATTCGTCCGTAGCTGAGCATTAAAGCCCCTAGAA ACTGTAGCAACATCG <u>A</u> GTGTTGCACAGATCGTGGCGGCTAAGTGGT CCAACAAACCCATCCTCCCGCGTTACCTTCGG	5637
		CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACCTAGCCGCC ACGATCTGTGCAACAC <u>T</u> GATGTTGCTACAGTTCTACGGGCTTTAA	5638
		TGCTCAGCTGACGGACGAAATTAGGAGGAA	
		GCAACATCG <u>A</u> GTGTTGA	5639
		TGCAACAC <u>T</u> GATGTTGC	5640
20	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT	TTCCCTCCTAATTCGTCCGTAGCTGAGCATTAAAGCCCCTAGAAA CTGTAGCAACATCG <u>A</u> GTGTTGCACAGATCGTGGCGGCTAAGTGGTC CAACAAACCCATCCTCCCGCGTTACCTTCGGC	5641
		GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACCTAGCCGC CACGATCTGTGCAACAC <u>T</u> GATGTTGCTACAGTTCTACGGGCTTTA	5642
		ATGCTCAGCTGACGGACGAAATTAGGAGGAA	
		CAACATCG <u>A</u> GTGTTGCAC	5643
		GTGCAACACATCGATGTTG	5644
25			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Met Overproduction CGS <i>Fragaria vesca</i> Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC TCAGCACCAAGGCC <u>A</u> CCGCAACTGCAGCAACATCGCGTCGCG CAGATCGTCGGCTCGTGGTCAACAAAGA	5645
	TCTTGTTGGACCACGAAGCCGCGACGATCTCGCGACGCCGAT GTTGCTGCAGTTGCGG <u>I</u> GGCCTGGTGC <u>T</u> GAGCTGGCGGACGA AGTTGGGAGGGAAAGCGGAGGGATGAGTGACGATA	5646
	CAAGGCC <u>A</u> CCGCAACT	5647
	AGTTGCGGTGGGCTTG	5648
10 Met Overproduction CGS <i>Fragaria vesca</i> Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAG GCCCGCCGCAACTGCA <u>A</u> CAACACATCGCGTCGCGCAGATCGTCG GGCTTCGTTGGTCCAACAAAGACTCCGACCTTC	5649
	GAAAGGTGGAGTCTTGTGGACCACGAAGCCGCGACGATCTG CGCGACGCCGATGTTG <u>T</u> GCAGTTGCGGCGGGCTTGGTGC <u>T</u> GA GCTGGCGGACGAAGTTGGGAGGGAAAGCGGAGGA	5650
	CAACTGCA <u>A</u> CAACATCG	5651
	CGATGTTG <u>T</u> GCAGTTG	5652
	TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG CAACTGCAACATC <u>A</u> CGCTCGCGCAGATCGTCGGCTTCG GGTCCAACAAAGACTCCGACCTTCGGCGGTGC GCACCGCCGAAAGGTGGAGTCTTGTGGACCACGAAGCCGCG ACGATCTCGCGCAGC <u>T</u> GATGTTGCTGCAGTTGCGGCGGGCCTT GGTGC <u>T</u> GAGCTGGCGGACGAAGTTGGGAGGGAA GCAACATC <u>A</u> CGCTCGCG CGCGACG <u>T</u> GATGTTGC	5653 5654 5655 5656
15 Met Overproduction CGS <i>Fragaria vesca</i> Gly80Ser GGC-AGC	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG AACTGCAACATC <u>G</u> ACGCTCGCGCAGATCGTCGGCTTCG GTCCAACAAAGACTCCGACCTTCGGCGGTGC	5657
	GGCACCGCCGAAAGGTGGAGTCTTGTGGACCACGAAGCCGCG GACGATCTCGCGCAGC <u>T</u> GATGTTGCTGCAGTTGCGGCGGGCCTT GGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	5658
	CAACATC <u>G</u> ACGCTCGCG	5659
	GCGCGACG <u>T</u> GATGTTG	5660
	TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCAGGCCAGC TAAGCACCAAGGCC <u>G</u> AGGCCGCAACTGCAGCAACATCGCGTCGCG CAAATCGTCGCCGCTCGTGGTCAACAAACAG	5661
20 Met Overproduction CGS <i>Glycine max</i> Arg68His CGC-CAC	CTGTTGTTGACCAACGAAGCGGCGACGATTGCGCGACGCCGAT GTTGCTGCAGTTGCGG <u>C</u> CGCCTGGTGC <u>T</u> AGCTGGCGCTGGA AGTTGGGAGGGAAAGCGGAGGGATGAGGGAGGGAGGA	5662
	CCAAGGCCGAGGCCGCAAC	5663

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTGCGGCTCGCCTTGG	5664
Met Overproduction CGS <i>Glycine max</i> Ser72Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAACGACCCAAG GCGCGCCGCAACTGCA <u>A</u> CAACATCGCGTCCGCAAATCGTCGC CGCTTCGTGGTCGAACAACAGCGACA <u>A</u> CTCTCC GGAGAGAGTTGTCGCTGTTGACCAACGAAGCGGCGACGATTG CGCGACGCCGATGTTG <u>T</u> TCAGTTGCGGCGCCTGGTGCTTA GCTGGCGCTGGAAGTTGGGAGGGAAAGCGGAGGA CAACTGCA <u>A</u> CAACATCG CGATGTTG <u>T</u> TCAGTTG	5665 5666 5667 5668
Met Overproduction CGS <i>Glycine max</i> Gly75Ser GGC-AGC	TCCCTCCCAACTTCCAGCGCCAGCTAACGACCCAAGGGCGGCCG CAACTGCA <u>A</u> CAACATCG <u>A</u> CGTCCGCAAATCGTCGCCGCTTCGT GGTCGAACAACAGCGACA <u>A</u> CTCTCCGGCCGCCG CGGCGGCCGGAGAGAGTTGTCGCTGTTGACCAACGAAGCGGC GACGATTGCGC <u>A</u> CG <u>T</u> CGATGTTGCTGCAGTTGCGGCCGCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA GCAACATCG <u>A</u> CGTCCGCG CGCGACG <u>T</u> CGATGTTG	5669 5670 5671 5672
Met Overproduction CGS <i>Glycine max</i> Gly75Asp GGC-GAC	TCCCTCCCAACTTCCAGCGCCAGCTAACGACCCAAGGGCGGCCG AACTGCA <u>A</u> CAACATCG <u>A</u> CGTCCGCAAATCGTCGCCGCTTCGT GTCGAACAACAGCGACA <u>A</u> CTCTCCGGCCGCCG CGGCGGCCGGAGAGAGTTGTCGCTGTTGACCAACGAAGCGGC GACGATTGCGC <u>A</u> CG <u>T</u> CGATGTTGCTGCAGTTGCGGCCGCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA CAACATCG <u>A</u> CGTCCGCG GCGCGACG <u>T</u> CGATGTTG	5673 5674 5675 5676
Met Overproduction CGS <i>Solanum tuberosum</i> Arg70His AGG-CAC	TGTCTTCTGATTTCAAGGTTCTCTCTAATTCTGAGGGCAGCT AAGCATTAAAGG <u>T</u> CA <u>C</u> AGGAATTGCAGCAATTGGCGTGGCTCA AGTTGTGGCGGCTTCTGGTCTAACACCCA TGGTTGTTAGACCAAGGAAGCCGCCACA <u>A</u> CTTGAGCCACGCCAATA TTGCTGCAATTCTG <u>T</u> GA <u>G</u> CCTTAATGCTTAGCTGCCTCACGAAAT TAGGAGGAAACCTGAAAATCAGAGAAAGACA TAAGG <u>T</u> CA <u>C</u> AGGAATT AATTCTG <u>T</u> GA <u>G</u> CCTTA	5677 5678 5679 5680
Met Overproduction CGS <i>Solanum tuberosum</i> Ser74Asn AGC-AAC	TTTCAGGTTCTCTCTAATTCTGAGGGCAGCTAACGATTAAGGC TAGGAGGAATTGCA <u>A</u> CAATTGGCGTGGCTCAAGTTGTGGCGG CTTCTGGTCTAACACCAAGCCGGCTCTGA TCAGGACCGGCTTGGTTAGACCAAGGAAGCCGCCACA <u>A</u> CTTG AGCCACGCCAATTG <u>T</u> GA <u>G</u> CAATTCTCTAGCCTTAATGCTTAGC TGCCTCACGAAATTAGGAGGAAACCTGAAAA	5681 5682

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GAATTGCAACAATATTG	5683
	CAATATTG <u>T</u> GCAATTG	5684
5 Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Ser GGC-AGC	TTCCCTCCTAATT <u>CGT</u> GAGGCAGCTAAC <u>GC</u> ATT <u>AGG</u> C <u>TTAGG</u> AGG AATT <u>GC</u> AG <u>CA</u> AT <u>AT</u> <u>AG</u> CG <u>GG</u> CT <u>CA</u> AG <u>TT</u> GT <u>GG</u> CG <u>GG</u> CT <u>CT</u> GG T <u>CTA</u> AC <u>AC</u> AC <u>CA</u> AG <u>CC</u> GG <u>CT</u> GA <u>TT</u> CA <u>CT</u> C	5685
	GAGTGAATT <u>CAGG</u> AC <u>CCGG</u> CT <u>GG</u> TT <u>GT</u> TA <u>GG</u> AC <u>CC</u> AG <u>GA</u> AG <u>CC</u> GC ACA <u>ACT</u> GT <u>AG</u> CC <u>AC</u> CG <u>CT</u> AA <u>AT</u> AT <u>TG</u> CT <u>GC</u> CA <u>AT</u> CC <u>CT</u> CT <u>AG</u> CC <u>TT</u> AA	5686
	GCA <u>AT</u> AT <u>TA</u> <u>AG</u> CG <u>GT</u> GG <u>CT</u>	5687
	AG <u>CC</u> AC <u>CG</u> CT <u>AA</u> AT <u>AT</u> GC	5688
	TTCCCTCCTAATT <u>CGT</u> GAGGCAGCTAAC <u>GC</u> ATT <u>AGG</u> C <u>TTAGG</u> AGG ATT <u>GC</u> AG <u>CA</u> AT <u>AT</u> <u>G</u> <u>AC</u> GT <u>GG</u> CT <u>CA</u> AG <u>TT</u> GT <u>GG</u> CG <u>GG</u> CT <u>CT</u> GG CT <u>TA</u> AC <u>AC</u> AC <u>CA</u> AG <u>CC</u> GG <u>CT</u> CT <u>GA</u> TT <u>CA</u> CT <u>CC</u>	5689
10 Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Asp GGC-GAC	GGAGTGAATT <u>CAGG</u> AC <u>CCGG</u> CT <u>GG</u> TT <u>GT</u> TA <u>GG</u> AC <u>CC</u> AG <u>GA</u> AG <u>CC</u> GC CACA <u>ACT</u> GT <u>AG</u> CC <u>AC</u> GT <u>CA</u> AT <u>AT</u> GT <u>GC</u> CA <u>AT</u> CC <u>CT</u> CT <u>AG</u> CC <u>TT</u> A	5690
	AT <u>GCT</u> TA <u>GG</u> CT <u>GC</u> CT <u>AC</u> GA <u>AA</u> AT <u>AGG</u> AG <u>GG</u> AA	
	CA <u>AT</u> AT <u>TA</u> <u>G</u> <u>AC</u> GT <u>GG</u> CT <u>C</u>	5691
	GAG <u>CC</u> AC <u>CG</u> <u>T</u> <u>CA</u> AT <u>AT</u> GT	5692
	CTTCCTCTCTTAT <u>CC</u> TC <u>CG</u> CT <u>CC</u> CC <u>AA</u> CT <u>TT</u> GT <u>CC</u> GT <u>CA</u> GT CAG <u>CA</u> CC <u>AA</u> GG <u>CT</u> CG <u>CC</u> <u>A</u> <u>CA</u> AC <u>CT</u> GC <u>AG</u> CA <u>AC</u> AT <u>GG</u> GT <u>TC</u> GC <u>AC</u> AG <u>GT</u> CG <u>TC</u> CG <u>CT</u> GC <u>CT</u> CT <u>GG</u> TC <u>CA</u> AC <u>AA</u> CT <u>TC</u>	5693
15 Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Arg73His CGC-CAC	GAG <u>TT</u> GT <u>GG</u> AC <u>CC</u> AG <u>GG</u> AG <u>GG</u> CG <u>AC</u> GC <u>AC</u> CT <u>GT</u> GC <u>GA</u> CC <u>AA</u> AT GT <u>GCT</u> GC <u>AG</u> TT <u>GT</u> GG <u>CG</u> AG <u>CC</u> CT <u>GG</u> GT <u>CT</u> GA <u>GC</u> TC <u>AG</u> GG <u>AC</u> AA AG <u>TT</u> GG <u>AG</u> GG <u>AA</u> AG <u>CG</u> GA <u>AG</u> GA <u>TA</u> AG <u>AG</u> AG <u>AG</u> GA <u>AG</u>	5694
	GG <u>CT</u> CG <u>CC</u> <u>A</u> <u>CA</u> AC <u>CT</u> GC <u>A</u>	5695
	T <u>GC</u> AG <u>TT</u> <u>G</u> <u>T</u> GG <u>CG</u> AG <u>CC</u>	5696
	TC <u>CT</u> TC <u>CG</u> CT <u>CC</u> CC <u>AA</u> CT <u>TT</u> GT <u>CC</u> GT <u>CA</u> GT <u>CT</u> CA <u>GC</u> AC <u>CA</u> AG <u>GG</u> CT <u>CG</u> CC <u>CG</u> CA <u>CT</u> GC <u>CA</u> <u>A</u> <u>CA</u> AC <u>AT</u> GG <u>GT</u> GT <u>CG</u> CA <u>CG</u> GT <u>CG</u> CT GC <u>CT</u> CT <u>GG</u> TC <u>CA</u> AC <u>AA</u> CT <u>CC</u> GT <u>AT</u> GC <u>CC</u> GG <u>CG</u>	5697
	GCG <u>CC</u> GG <u>CA</u> TC <u>GG</u> AG <u>TT</u> GT <u>GG</u> AC <u>CC</u> AG <u>GG</u> AG <u>GG</u> CG <u>CG</u> AC <u>GC</u> AC <u>CT</u> GT <u>GC</u> GA <u>CC</u> AA <u>AT</u> GT <u>G</u> <u>T</u> GC <u>AG</u> TT <u>GT</u> GG <u>CG</u> AG <u>CC</u> CT <u>GG</u> GT <u>CT</u> G AG <u>CT</u> GA <u>CG</u> GA <u>AA</u> GT <u>TT</u> GG <u>AG</u> GG <u>AA</u> AG <u>CG</u> GA <u>AG</u> GA	5698
20 Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Ser77Asn AGC-AAC	CA <u>AC</u> TC <u>GC</u> <u>CA</u> <u>A</u> <u>CA</u> AC <u>AT</u> TT <u>G</u>	5699
	CA <u>AT</u> GT <u>TT</u> <u>G</u> <u>T</u> GC <u>AG</u> TT <u>G</u>	5700

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Gly80Ser GGT-AGT	TTCCCTCCCAACTTTGCCGTAGCTCAGCACCAAGGGCTGCCGC AACTGCAGCAACATT <u>AGT</u> GTGCGACAGGTCGCTGCCTCCTG GTCCAACAACACTCCGATGCCGGGCCACCTCTT	5701
	AAGAGGTGGCGCCGGCATCGGAGTTGGACCAAGGAGGCAGC GACGACCTGTGCGACACT <u>AAT</u> GTGCTGCAGTTGCCGGAGCCT TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	5702
	GCAACATT <u>AGT</u> GTGCGCA	5703
	TGCGACACT <u>AAT</u> GTGTC	5704
10 Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Gly80Asp GGT-GAT	TTCCCTCCCAACTTTGCCGTAGCTCAGCACCAAGGGCTGCCGCA ACTGCAGCAACATT <u>GAT</u> GTGCGACAGGTCGCTGCCTCCTGG TCCAACAACACTCCGATGCCGGGCCACCTCTT	5705
	CAAGAGGTGGCGCCGGCATCGGAGTTGGACCAAGGAGGCAG CGACGACCTGTGCGACAT <u>CAAT</u> GTGCTGCAGTTGCCGGAGCC TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	5706
	CAACATT <u>GAT</u> GTGCGAC	5707
	GTGCGACAT <u>CAAT</u> GTG	5708
	CCTCTGCTACCATCCTCCGCTTCCGCCAAACTTTGCCAGCTTAGCACCAAGG TTAGCACCAAGGCAC <u>ACCGCA</u> CTGCAGCACACATGGCGTCGCG CAGATCGTCGCCGCCGCGTGGTCCGACTGCC	5709
15 Met Overproduction CGS <i>Zea mays</i> Arg41His CGC-CAC	GGGCAGTCGGACCACGCCGGCGACGATCTGCACGCC TGGTGCAGTTGG <u>GTG</u> CCCTGGTCTAAGCTGGCGACA AAGTTGGCGAAAGCGGAGGATGGTAGCAGAGG	5710
	CAAGGCAC <u>ACCGCA</u> CT	5711
	AGTTGG <u>GTG</u> CCCTTG	5712
	TCCTCCGCTTCCGCCAAACTTTGCCAGCTTAGCACCAAGG CACGCCGCAACTGCA <u>ACAAC</u> ATGGCGTCGCCAGATCGTCGCC	5713
20 Met Overproduction CGS <i>Zea mays</i> Ser45Asn AGC-AAC	GGGCAGCGGGCGGGCAGTCGGACCACGCCGGCGACGATC TGCACGCCGAT <u>GTG</u> TCAGTTGCCGGCGTGCCTGGTCT AAGCTGGCGAACAAAGTTGGCGAAAGCGGAGGA	5714
	CAACTGCA <u>ACAAC</u> ATCG	5715
	CGAT <u>GTG</u> TCAGTTG	5716
	TTCCGCCAAACTTTGCCAGCTTAGCACCAAGGCACGCC AACTGCAGCAACAT <u>CAG</u> CGTCGCCAGATCGTCGCCGCCGTG GTCCGACTGCCGCCGCTGCCACTTAG	5717
25 Met Overproduction CGS <i>Zea mays</i> Gly48Ser GGC-AGC	CTAAGTGGGGCGAGCGGGGGCAGTCGGACCACGCCGG CGACGATCTGCCGACGCTGAT <u>GTG</u> CTGCAGTTGCCGGCGTGC TTGGTGCTAACGCTGGCGAACAAAGTTGGCGAAA	5718
	GCAACAT <u>CAG</u> CGTCGCC	5719

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CGCGACGCT <u>G</u> ATGTTGC	5720
Met Overproduction CGS <i>Zea mays</i> Gly48Asp GGC-GAC	TTCCGCCAAACTTGTCCGCCAGCTAGCACCAAGGCACGCCGC AACTGCAGCAACATCG <u>A</u> CGTCGCGCAGATCGTCGCCGCCGCGT GTCCGACTGCCGCCGCTCGCCCCACTTAGG	5721
	CTTAAGTGGGGCGAGCGGGGGCAGTCGGACCACGCGCG GCGACGATCTGC <u>G</u> CGACG <u>T</u> CGATGTTGCTGCAGTTGCCGCGTGC CTTGGTGCTAAGCTGGCGACAAAGTTGGCGGAA	5722
	CAACATCG <u>A</u> CGTCGCGC	5723
	GCGCGACG <u>T</u> CGATGTTG	5724
Met Overproduction TS <i>Arabidopsis thaliana</i> Leu205Arg CTT-CGT	GTATGAATGATCTGGGTGAAACACTGTGGGATTAGTCATA GAAGTTCAAGGATCG <u>T</u> GGATGACTGTTGGTAGTCAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT	5725
	ACCACAGGTGTTTCATCTTCTCAGACGATTAAC AAACAGTCATTCC <u>A</u> CGATCCTGAAACTCCTGTATGACTAACCA ACAGTGTTCACCCACAGATCATTAC	5726
	CAAGGATCG <u>T</u> GGATGA	5727
	TCATTCC <u>A</u> CGATCCTG	5728
Met Overproduction TS <i>Solanum tuberosum</i> Leu198Arg CTT-CGT	GCATGACTGATTGGGTCAAACACTGTGGGATTAGCCATA GTAGTTTAAGGATCG <u>T</u> GGATGACTGTTGGTAGTCAGTTAA TCGCTTGC <u>G</u> GGAAAATGCATAAACCGGTTGT	5729
	ACAACCGGTTATGCATTTCCGAAGCGATTAAC AAACAGTCATCCC <u>A</u> CGATCCTAAA ACAGTGTGACCCACAAATCAGTCATGC	5730
	TAAGGATCG <u>T</u> GGGATGA	5731
	TCATCCC <u>A</u> CGATCCTA	5732
Lys Overproduction DHPS <i>Zea mays</i> Ser157Asn AGC-AAC	TCATGGGCACACAGTGAAC TAGGCAACACAGGAA <u>A</u> CAACTCAAC ACAGAACAGGATTGCTGGCATGCATGC	5733
	GCATGCATGCCAACAGCAA TCTCTGGTTGAGTTG <u>T</u> TCCTGTGTTGCCTATCA AGCCAAAGCAGTC CACAGGAA <u>A</u> CAACTCAA	5734
	TTGAGTTG <u>T</u> TCCTGTG	5735
	GCTCTAGAATCAAAGTGA GAGAACGGCGTCCACG <u>A</u> ACAGAACAGG CATGCGGCTCTCCACATCA	5736
Lys Overproduction DHPS <i>Zea mays</i> Ala166Val GCA-GAA	GAGAACAGGATTGATGTGGAGAGCCGCATGC AAATCCCTGTTCTG <u>T</u> CGTGGACGGCTCT CCTGTGTTGCCTATCA	5737
	GAGAACAGGATTGATGTGGAGAGCCGCATGC AAATCCCTGTTCTG <u>T</u> CGTGGACGGCTCT CCTGTGTTGCCTATCA	5738

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGTCCACG <u>AA</u> ACAGAAC	5739
	GT <u>T</u> CTGTT <u>T</u> CGTGGACG	5740
Lys Overproduction DHPS <i>Zea mays</i> Ala166Thr GCA-ACA	GGCTCTAGAACAA <u>AGT</u> GATAGGCAACACAGGAAGCAACTCAACC AGAGAAGCCGTCCACACAA <u>ACAGAAC</u> AGGGATTGCTGTTGGCAT GCATGCGGCTCTCACATCAATCCTTACTACG	5741
	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCAA ATCCCTGTTCTGTT <u>G</u> GTGGACGGCTCTGGTTGAGTTGCTTC CTGTGTTGCCTATCACTTGATTCTAGAGCC	5742
	CCGTCCAC <u>ACA</u> ACAGAA	5743
	TTCTGTT <u>G</u> GTGGACGG	5744
Lys Overproduction DHPS <i>Oryza sativa</i> Ser124Asn AGT-AAT	TTATTGGGCATACAG <u>TT</u> ACTGCT <u>TT</u> GGCACTAAA <u>TTAA</u> AGTGGT CGGCAACACAG <u>AA</u> ATA <u>ACT</u> CAACAA <u>AGGGAGG</u> CTATT <u>ACG</u> CAAC TGAGCAGGGATT <u>CG</u> CTG <u>TA</u> GGTAT <u>GC</u> ACGC	5745
	GC <u>GT</u> GCATAC <u>CT</u> ACAG <u>CG</u> GA <u>AT</u> CC <u>CT</u> G <u>CT</u> CAG <u>TT</u> GC <u>GT</u> GA <u>AT</u> AGCC TCC <u>CT</u> GTTGAG <u>TT</u> A <u>TT</u> CC <u>CT</u> GTTG <u>CC</u> GACC <u>AC</u> TT <u>TA</u> AT <u>TT</u> AGT GCC <u>AA</u> AG <u>CA</u> G <u>TT</u> ACT <u>GT</u> T <u>AT</u> GC <u>CC</u> A <u>ATA</u> A	5746
	CACAG <u>GG</u> <u>AA</u> <u>TA</u> ACT <u>CAA</u>	5747
	TTGAG <u>TT</u> A <u>TT</u> CC <u>CT</u> G <u>TG</u>	5748
Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Val GCA-GTA	GCA <u>CT</u> AAA <u>TT</u> AA <u>AG</u> TGG <u>TC</u> GG <u>CA</u> ACACAG <u>GA</u> AG <u>TA</u> ACT <u>CA</u> ACAA GG <u>GG</u> AG <u>GG</u> CTATT <u>CA</u> <u>CG</u> <u>TA</u> CT <u>GA</u> G <u>AC</u> G <u>AG</u> GG <u>AT</u> TC <u>CG</u> <u>CT</u> G <u>T</u> AG <u>GT</u> T <u>AT</u> G CAC <u>GC</u> GG <u>CT</u> CT <u>CC</u> AC <u>AT</u> CA <u>AT</u> C <u>CT</u> T <u>ACT</u> AC <u>GG</u>	5749
	CCGTAGTAAGGATTGATGTGGAGAGCC <u>CG</u> <u>GT</u> <u>GC</u> <u>AT</u> AC <u>CT</u> AC <u>AG</u> <u>CG</u> GA <u>AT</u> CC <u>CT</u> G <u>CT</u> CAG <u>TT</u> <u>AC</u> <u>GT</u> <u>GA</u> <u>AT</u> AG <u>CC</u> <u>CT</u> <u>CC</u> <u>CT</u> G <u>TT</u> G <u>AG</u> <u>TT</u> <u>AC</u> <u>TT</u> C <u>CT</u> G <u>TT</u> G <u>CC</u> GACC <u>AC</u> TT <u>TA</u> AT <u>TT</u> AG <u>GT</u> <u>GC</u>	5750
	TATT <u>CA</u> <u>CG</u> <u>TA</u> CT <u>GA</u> <u>GC</u>	5751
	G <u>CT</u> CAG <u>TT</u> <u>AC</u> <u>GT</u> <u>GA</u> <u>AT</u> A	5752
Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Thr GCA-ACA	GG <u>CA</u> CT <u>AA</u> <u>AA</u> <u>TT</u> AA <u>AG</u> TGG <u>TC</u> GG <u>CA</u> ACACAG <u>GA</u> AG <u>TA</u> ACT <u>CA</u> ACAA AG <u>GG</u> AG <u>GG</u> CTATT <u>CA</u> <u>CA</u> <u>AC</u> <u>CT</u> <u>GA</u> <u>AG</u> <u>GC</u> <u>AG</u> <u>GG</u> <u>AT</u> TC <u>CG</u> <u>CT</u> G <u>T</u> AG <u>GT</u> T <u>AT</u> G GC <u>AC</u> <u>GC</u> GG <u>CT</u> CT <u>CC</u> AC <u>AT</u> CA <u>AT</u> C <u>CT</u> T <u>ACT</u> AC <u>AG</u> <u>CG</u>	5753
	CGTAGTAAGGATTGATGTGGAGAGCC <u>CG</u> <u>GT</u> <u>GC</u> <u>AT</u> AC <u>CT</u> AC <u>AG</u> <u>CG</u> AA <u>AT</u> CC <u>CT</u> G <u>CT</u> CAG <u>TT</u> <u>G</u> <u>TA</u> <u>GT</u> <u>GA</u> <u>AT</u> AG <u>CC</u> <u>CT</u> <u>CC</u> <u>CT</u> G <u>TT</u> G <u>AG</u> <u>TT</u> <u>AC</u> <u>TC</u> C <u>CT</u> G <u>TT</u> G <u>CC</u> GACC <u>AC</u> TT <u>TA</u> AT <u>TT</u> AG <u>GT</u> <u>GC</u>	5754
	CTATT <u>CA</u> <u>CA</u> <u>AC</u> <u>TG</u> <u>AG</u>	5755
	CTCAG <u>TT</u> <u>G</u> <u>GT</u> <u>GA</u> <u>AT</u> <u>AG</u>	5756
Lys Overproduction DHPS 1 <i>Triticum aestivum</i>	TCAT <u>CG</u> <u>GG</u> CAT <u>AC</u> <u>TG</u> <u>TT</u> AA <u>CT</u> <u>G</u> <u>CT</u> <u>TT</u> GG <u>AG</u> <u>CC</u> <u>AA</u> <u>CA</u> <u>CT</u> <u>AA</u> <u>AG</u> <u>GT</u> <u>AT</u> AG <u>GC</u> <u>AA</u> <u>AC</u> <u>CG</u> <u>GG</u> <u>AA</u> <u>TA</u> <u>AC</u> <u>TC</u> <u>AA</u> <u>CC</u> <u>AG</u> <u>AG</u> <u>AA</u> <u>AG</u> <u>CT</u> <u>G</u> <u>TT</u> <u>CA</u> <u>CG</u> <u>CG</u> <u>GA</u> C <u>AG</u> <u>AG</u> <u>CG</u> <u>GG</u> <u>AT</u> <u>TT</u> <u>G</u> <u>CT</u> <u>G</u> <u>TT</u> <u>GG</u> <u>C</u> <u>AT</u> <u>G</u> <u>C</u> <u>AT</u> <u>G</u> <u>C</u>	5757
Ser165Asn AGT-AAT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCATGCATGCCAACAGCAAATCCCTGCTCTGTCGCGTGAACAGCTCTCTGGTGTGAGTTAATGTTGGCTCCAAAGCAGTTAACAGTATGCCCGATGA	5758
	CACGGGAA <u>A</u> TAACCTCAA	5759
	TTGAGTTA <u>T</u> TCCTCGT	5760
5 Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Val GCG-GTG	GAGCCAACATTAAGTGTAGGCAACACGGGAAGTAACCTCAACCA GAGAAGCTGTTACCGT <u>G</u> ACAGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTTCATGTCAATCCTTACTACGG	5761
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTC <u>AC</u> GTGAACAGCTTCTGGTTGAGTTACTT CCCGTGTGCTATCACTTAATGTTGGCTC	5762
	TGTTCAC <u>CG</u> TGACAGAGC	5763
	GCTCTGTC <u>AC</u> GTGAACA	5764
	GGAGCCAACATTAAGTGTAGGCAACACGGGAAGTAACCTCAACC AGAGAAGCTGTTAC <u>AC</u> CGACAGAGCAGGGATTGCTGTTGGCAT GCATGCAGCTCTTCATGTCAATCCTTACTACGG	5765
10 Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Thr GCG-ACG	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTC <u>CG</u> GTGAACAGCTTCTGGTTGAGTTACTTC CCGTGTGCTATCACTTAATGTTGGCTC	5766
	CTGTTCAC <u>AC</u> GTGACAGAG	5767
	CTCTGTC <u>CG</u> GTGAACAG	5768
	TCATCGGGCACACTGTTACTGCTTGGAACTAACATTAAGTGTAGGCAACACGGGAAGTAACCTCAACTAGAGAAGCGATTACGCTTC AGAGCAGGGATTGCTGTTGGCATGCATGC	5769
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT TCTCTAGTTGAGTTA <u>T</u> TCCTCGTGTGCTATCACTTAATGTTAGT TCCAAAGCAGTTAACAGTGTGCCCGATGA	5770
15 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ser154Asn AGT-AAT	CACGGGAA <u>A</u> TAACCTCAA	5771
	TTGAGTTA <u>T</u> TCCTCGT	5772
	GAACTAACATTAAGTGTAGGCAACACGGGAAGTAACCTCAACTAGAGCAGGGATTGCTGTTGGCATGC ATGCAGCTCTCCATGTCAATCCTTACTATGG	5773
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAA <u>AC</u> GTGAATCGCTCTAGTTGAGTTACTTC CCGTGTGCTATCACTTAATGTTAGTTC	5774
	GATTCA <u>CG</u> TTCAGAGC	5775
20 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Val GCT-GTT	GCTCTGAA <u>AC</u> GTGAATC	5776

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Thr GCT-ACT	GGAACTAACATTAAGTGTAGGCAACACAGGGAAAGTAACCTCAACT AGAGAAGCGATTCAC <u>ACTT</u> CAGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTCCATGTCAATCCTTACTATG	5777
	CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGAAG <u>TGT</u> GAATCGCTCTAGTTGAGTTACTTCC CGTGTGCTATCACTTAATGTTAGTTCC	5778
	CGATT <u>CAC</u> <u>ACTT</u> CAGAG	5779
	CTCTGAAG <u>TGT</u> GAATCG	5780
10 Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ser154Asn AGT-AAT	CTCATTGGGCATACTGTGAACGTGCTTGGCTCTAGAATTAAAGTGA TAGGCAACACAGGAA <u>ATA</u> ACTCAACCAGAGAAGCTGTTGGCATGC CAGAGCAGGGATTGCTGTTGGCATGCATG	5781
	CATGCATGCCAACAGCAA <u>AT</u> CCCTGCTCTGTTGGCTAACAGC CTCTGGTTGAGTT <u>ATT</u> CCCTGTGTTGCCTATCACTTAATTCTAGA GCCAAAGCAGTTCACAGTATGCCAACATGAG	5782
	CACAGGAA <u>ATA</u> ACTCAA	5783
	TTGAGTT <u>ATT</u> CCCTGTG	5784
	GCTCTAGAATTAAAGTGTAGGCAACACAGGAAGTAACCTAACCA GAGAAGCTGTT <u>CACG</u> <u>T</u> ACAGAGCAGGGATTGCTGTTGGCATGC ATGCAGCTCTCCACATCAATCCTTACTATGG	5785
15 Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Val GCA-GTA	CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTT <u>ACGT</u> GAACAGCTCTCTGGTTGAGTTACTTC CTGTGTTGCCTATCACTTAATTCTAGAGC	5786
	TGTTCACG <u>T</u> ACAGAGC	5787
	GCTCTGTT <u>ACGT</u> GAACA	5788
	Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Thr GCA-ACA	5789
20 Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Thr GCA-ACA	GGCTCTAGAATTAAAGTGTAGGCAACACAGGAAGTAACCTAAC AGAGAAGCTGTT <u>CAC</u> <u>ACA</u> ACAGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTCCACATCAATCCTTACTATG	5790
	CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTT <u>GT</u> GAACAGCTCTCTGGTTGAGTTACTTC TGTGTTGCCTATCACTTAATTCTAGAGCC	5791
	CTGTTCAC <u>ACA</u> ACAGAG	5792
	CTCTGTT <u>GT</u> GAACAG	5793
25 Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ser136Asn AGC-AAC	TCATTGGTCACACAGTCATTGTTGGAGGGCCATCAAAGTCAT CGGGAACACTGGAA <u>ACA</u> ACTCCACAAGGGAAAGCAATCCATGCAA CTGAACAGGGATTGCTGTAGGTATGCATGC	5794
	GCATGCATACCTACAGCAA <u>AT</u> CCCTGTT <u>GT</u> CAGTTGCATGGATTGCTT CCCTTGTGGAGTT <u>GT</u> CCAGTGTCCC <u>GT</u> ACTTTGATGGACC CTCCAAAACAATTGACTGTGTGACCAATGA CACTGGAA <u>ACA</u> ACTCCA	5795

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TGGAGTTG <del>T</del> CCAGTG	5796
5 Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGAACACTGGAAGCAACTCCACAA GGGAAGCAATCCATG <del>T</del> ACTGAACAGGGATTGCTGTAGGTATGC ATGCAGCTCTTACATTAATCCCTACTATGG	5797
	CCATAGTAGGGATTAAATGTGAAGAGCTGCATGCATACCTACAGCA AATCCCTGTT <del>C</del> AGTT <del>A</del> CATGGATTGCTCCCTGTGGAGTTGCTTC CAGTGT <del>T</del> CCCGATGACTTTGATGGACCCCTC	5798
	AATCCATG <del>T</del> AACTGAAC	5799
	GTT <del>C</del> AGTT <del>A</del> CATGGATT	5800
	GGAGGGTCCATCAAAGTCATCGGAACACTGGAAGCAACTCCAC AAGGGAAAGCAATCCAT <del>A</del> CAACTGAACAGGGATTGCTGTAGGTAT GCATGCAGCTCTTACATTAATCCCTACTATG	5801
10 Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Thr GCA-ACA	CATAGTAGGGATTAAATGTGAAGAGCTGCATGCATACCTACAGCAA ATCCCTGTT <del>C</del> AGTT <del>G</del> ATGGATTGCTCCCTGTGGAGTTGCTTC AGTGT <del>T</del> CCCGATGACTTTGATGGACCCCTC	5802
	CAATCCAT <del>A</del> CAACTGAA	5803
	TTCAGTTG <del>T</del> ATGGATTG	5804
	TTATAGGCCATACCGTTAAC <del>T</del> GTTGGCGGAAGCATCAAAGTCAT TGGAAACACTGGAA <del>A</del> CAATTGACTAGAGAAGCAATCCACCGCGAC TGAACAAAGGATTCCGGTGGAAATGCATGC	5805
	GCATGCATTCCAACCGCGAATCCTGTT <del>C</del> AGTCGCGTGGATTGCT TCTCTAGTCGAATTG <del>T</del> CCAGTGT <del>T</del> CCAATGACTTTGATGCTTC CGCCAAACAGTTAACGGTATGGCCTATAA	5806
15 Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ser142Asn AGC-AAC	CACTGGAA <del>A</del> CAATTGCA	5807
	TCGAATTG <del>T</del> CCAGTG	5808
	GGCGGAAGCATCAAAGTCATTGGAACACTGGAAGCAATTGACTA GAGAAGCAATCCACG <del>T</del> ACTGAACAAGGATTCCGGTGGAAATGC	5809
	ATGCTGCTCTTACATATAAACCTTACTATGG	
	CCATAGTAAGGGTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCC <del>T</del> GGATTGCTCTAGTCGAATTGCTTC CAGTGT <del>T</del> CCAATGACTTTGATGCTTC	5810
20 Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Val GCG-GTG	AATCCACG <del>T</del> ACTGAAC	5811
	GTT <del>C</del> AGTC <del>A</del> CGTGGATT	5812
	GGCGGAAGCATCAAAGTCATTGGAACACTGGAAGCAATTGACT AGAGAAGCAATCCAC <del>A</del> CGACTGAACAAGGATTCCGGTGGAAATG CATGCTGCTCTTACATATAAACCTTACTATG	5813
	CATAGTAAGGGTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCCTTGGATTGCTCG <del>T</del> GTGGATTGCTCTAGTCGAATTGCTTC	5814
	AGTGT <del>T</del> CCAATGACTTTGATGCTTC	
25		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAATCCAC <u>AC</u> GA <u>CT</u> GAA	5815
	TTCAGTC <u>GG</u> GTGGATTG	5816
5 Lys Overproduction DHPS <i>Glycine max</i> Ser103Asn AGC-AAC	TTATTGCTCATACAGTC <u>AA</u> CTG <u>TT</u> GGTGGAAAATT <u>AAGG</u> TTATT <u>GG</u> GGAA <u>AA</u> ACTGGAA <u>AC</u> AA <u>CT</u> CCACCAGGGAA <u>GC</u> ATT <u>CAT</u> G <u>CC</u> ACT GAGCAGGG <u>TT</u> T <u>G</u> CT <u>G</u> TA <u>AT</u> GCATGC GCAT <u>G</u> C <u>AT</u> CC <u>AA</u> AC <u>AG</u> CAAA <u>AC</u> CC <u>CT</u> G <u>CT</u> C <u>AG</u> T <u>GG</u> C <u>AT</u> GA <u>AT</u> TG <u>G</u> C <u>T</u> TCC <u>CT</u> GG <u>GG</u> AG <u>TT</u> G <u>TT</u> CC <u>AG</u> T <u>TT</u> CC <u>AA</u> AT <u>AA</u> CC <u>CT</u> TA <u>AT</u> TT <u>CC</u> CAC <u>CC</u> AA <u>AC</u> AG <u>TT</u> ACT <u>GT</u> T <u>AT</u> G <u>AG</u> CA <u>AA</u> AA TAC <u>TG</u> GA <u>AA</u> AC <u>AC</u> CT <u>CC</u> TGGAG <u>TT</u> G <u>TT</u> CC <u>AG</u> TA	5817 5818 5819 5820
10 Lys Overproduction DHPS <i>Glycine max</i> Ala112Val GCC-GTC	GTGGGAAAATT <u>AAGG</u> TTATT <u>GG</u> AA <u>AT</u> ACT <u>GG</u> AA <u>AG</u> CA <u>AC</u> CC <u>AC</u> CA GG <u>GA</u> AG <u>CA</u> ATT <u>CAT</u> G <u>T</u> <u>CA</u> CT <u>G</u> AG <u>C</u> AG <u>GG</u> <u>TT</u> T <u>G</u> CT <u>G</u> TT <u>GG</u> AA <u>AT</u> GC AT <u>G</u> CT <u>G</u> CC <u>CT</u> TC <u>AC</u> AT <u>AA</u> AC <u>CC</u> CT <u>TA</u> CT <u>AT</u> GG CC <u>AT</u> AG <u>TA</u> AG <u>GG</u> <u>TT</u> T <u>AT</u> GT <u>GA</u> AG <u>GG</u> C <u>AG</u> C <u>AT</u> G <u>C</u> ATT <u>CC</u> AA <u>AG</u> CA AA <u>AC</u> CC <u>CT</u> G <u>CT</u> C <u>AG</u> T <u>GG</u> <u>T</u> <u>AT</u> GA <u>AT</u> TG <u>CT</u> CC <u>CT</u> GG <u>AG</u> TT <u>G</u> CT <u>TC</u> CC <u>AG</u> T <u>AT</u> TT <u>CC</u> AA <u>AT</u> AA <u>CC</u> TT <u>TA</u> AT <u>TT</u> CC <u>CC</u> AC AATT <u>CAT</u> G <u>T</u> <u>CA</u> CT <u>G</u> AG <u>C</u> G <u>CT</u> C <u>AG</u> T <u>G</u> <u>AC</u> AT <u>GA</u> ATT <u>G</u>	5821 5822 5823 5824
15 Lys Overproduction DHPS <i>Glycine max</i> Ala112Thr GCC-ACC	GGTGGGAAAATT <u>AAGG</u> TTATT <u>GG</u> AA <u>AT</u> ACT <u>GG</u> AA <u>AG</u> CA <u>AC</u> CC <u>AC</u> CA AG <u>GG</u> GA <u>AG</u> CA <u>AT</u> TC <u>AT</u> <u>AC</u> CA <u>CT</u> G <u>AG</u> C <u>AG</u> GG <u>TT</u> T <u>G</u> CT <u>G</u> TT <u>GG</u> AA <u>AT</u> G CAT <u>G</u> CT <u>G</u> CC <u>CT</u> TC <u>AC</u> AT <u>AA</u> AC <u>CC</u> CT <u>TA</u> CT <u>AT</u> AT <u>G</u> CAT <u>AG</u> T <u>TA</u> AG <u>GG</u> <u>TT</u> T <u>AT</u> GT <u>GA</u> AG <u>GG</u> C <u>AG</u> C <u>AT</u> G <u>C</u> ATT <u>CC</u> AA <u>AG</u> CA AA <u>CC</u> CT <u>G</u> CT <u>CA</u> GT <u>GG</u> <u>T</u> <u>AT</u> GA <u>AT</u> TG <u>CT</u> CC <u>CT</u> GG <u>AG</u> TT <u>G</u> CT <u>TC</u> CAG <u>T</u> <u>AT</u> TT <u>CC</u> AA <u>AT</u> AA <u>CC</u> TT <u>TA</u> AT <u>TT</u> CC <u>CC</u> AC CAATT <u>CAT</u> <u>AC</u> CA <u>CT</u> G <u>AG</u> CT <u>CA</u> GT <u>GG</u> <u>T</u> <u>AT</u> GA <u>AT</u> TG	5825 5826 5827 5828
20 Trp Overproduction AS <i>Arabidopsis thaliana</i> Asp341Asn GAC-AAC	CTTGC <u>AG</u> GA <u>GA</u> CA <u>AT</u> TT <u>CAG</u> AT <u>CG</u> T <u>G</u> CT <u>G</u> AG <u>T</u> CA <u>AC</u> G <u>TT</u> T <u>G</u> AG CG <u>GC</u> GA <u>AC</u> AT <u>TT</u> G <u>CA</u> <u>AA</u> AC <u>CC</u> CT <u>TT</u> GA <u>AG</u> TT <u>AT</u> AG <u>AG</u> CA <u>CT</u> A <u>AG</u> A G <u>TT</u> GT <u>GA</u> AT <u>CC</u> AA <u>AG</u> T <u>CC</u> GT <u>AT</u> AT <u>GG</u> TT <u>AT</u> AATA <u>AC</u> CC <u>CA</u> T <u>AT</u> AC <u>GG</u> ACT <u>TT</u> GG <u>AT</u> TC <u>AC</u> CA <u>CT</u> T <u>TA</u> GT <u>G</u> CT <u>CT</u> T <u>AT</u> AA <u>CT</u> TC <u>AA</u> AG <u>GG</u> <u>TT</u> T <u>G</u> CA <u>AT</u> GT <u>TC</u> CG <u>CC</u> GT <u>CA</u> AA <u>AC</u> GT <u>TG</u> ACT CAG <u>GC</u> AC <u>GA</u> T <u>CT</u> GA <u>AA</u> AT <u>AT</u> GT <u>CT</u> CC <u>CT</u> G <u>CA</u> AG CATT <u>G</u> CA <u>AA</u> AC <u>CC</u> CT <u>TT</u> AA <u>AG</u> GG <u>GG</u> <u>TT</u> T <u>G</u> CA <u>AT</u> GT	5829 5830 5831 5832
25 Trp Overproduction AS <i>Nicotiana tabacum</i> Asp326Asn GAC-AAC	GCTGC <u>AG</u> GA <u>GA</u> CA <u>AT</u> TT <u>CAG</u> AT <u>CG</u> T <u>G</u> CT <u>G</u> AG <u>T</u> CA <u>AC</u> G <u>CT</u> T <u>G</u> AG <u>A</u> GA <u>AG</u> GA <u>AC</u> AT <u>TT</u> G <u>CA</u> <u>AA</u> AC <u>CC</u> AT <u>TT</u> GA <u>AG</u> GT <u>T</u> AC <u>AG</u> AG <u>C</u> AT <u>TA</u> AG <u>A</u> T <u>G</u> TA <u>AT</u> CC <u>AA</u> AG <u>CC</u> CA <u>AT</u> AT <u>G</u> ACT <u>T</u> AC <u>A</u>	5833

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTAAGTCATATATGGGCTGGATTACAATTCTTAATGCTCTGTA CACTTCAAATGGGT <u>T</u> AGCAAATGTTCTCTCAAAGCGTTGACTT AAAACGATTGAAATATGTCTCCTGCAGC	5834
	CATTTGCT <u>A</u> CCCCATT	5835
	AAATGGGT <u>T</u> AGCAAATG	5836
5 Trp Overproduction AS <i>Oryza sativa</i> Asp323Asn GAC-AAC	CTAGCTGGTGCACATTTCAAGTAGTCTTAAGCCAGCGTTTGAGA GGCGTACATTGCT <u>A</u> CCCCTTGAGGTGTACCGTGCATTGCGTA TTGTCATCCTAGTCCTTATATGGCCTATC	5837
	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAAGGGT <u>T</u> AGCAAATGTACGCCCTCTAAAACGCTGGC TTAAGACTACTTGAAAATGTCACCAAGCTAG	5838
	CATTTGCT <u>A</u> CCCCTTT	5839
	AAAGGGT <u>T</u> AGCAAATG	5840
	CTTGGCTGGTGCACATATTCCAGATCGTACTAAGTCAGCGTTTGAAA GGCGAACGTTCGCA <u>A</u> CCCCATTGAAATCTATAGATCACTGAGGA TTGTTAACCAAGCCCATAATGACTTATT	5841
10 Trp Overproduction AS <i>Ruta graveolens</i> Asp354Asn GAC-AAC	AATAAGTCATATATGGGCTGGATTACAATCCTCAGTGTACTATA GATTCAATGGGT <u>T</u> GC <u>A</u> CGTTGCCCTTCAAAACGCTGACTT AGTACGATCTGGAATATGTCACCAAGCAAG	5842
	CGTTCGCA <u>A</u> CCCCATT	5843
	AAATGGGT <u>T</u> GC <u>A</u> ACG	5844
	CTGGCTGGGACATATTCCAGCTTGTCTTAAGTCAGCGTTGAA CGGCGAACATTGCA <u>A</u> ATCCATTGAAGTCTACCGAGCATTGAGA ATTGTCAACCCAA <u>G</u> TCCATAATGACTTATT	5845
	AATAAGTCATATATGGACTTGGGTGACAATTCTCAATGCTCGGT GACTTCAAATGGAT <u>T</u> GC <u>A</u> ATGTTGCCGTTCAAACGCTGACTT AGGACAAGCTGGAATATGTC <u>CCC</u> AGCCAG	5846
15 Trp Overproduction AS <i>Catharanthus roseus</i> Asp354Asn GAT-AAT	CATTTGCA <u>A</u> ATCCATT	5847
	AAATGGAT <u>T</u> GC <u>A</u> ATG	5848

**Example 10****Production of modified starch in plants**

A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, 5 polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules 10 which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of  $\alpha$ -1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional  $\alpha$ -1,6-glycosidic linkages. In plants from 15 which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunken* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain 20 quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

**Table 20**  
**Genome-Altering Oligos Conferring Increased Starch**

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Ala99Lys GCA-AAA	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGGAGGTGG <u>AAA</u> AGGAACTCGACTCTTCCTCTCACAAAA CGCCGCGCCAAGCCTGCCGTTCCATCGGGG	5849
	CCCCGATAGGAACGGCAGGCTTGGCGCGGGCTTTGTGAGAGGA AAGAGTCGAGTCC <u>TTT</u> CCACCTCCAAGAATAATGGAAGCAACT GTCCTTGGATCC <u>TTT</u> CTCAGTCTCAAGTTC	5850
	GAGGTGG <u>AAA</u> AGGAAC	5851
	AGTTCC <u>TTT</u> CCACCTC	5852
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro127Leu CCA-CTA	CAAAACGCCGCGCCAAGCCTGCCCTATCGGGGGAGCCTAT AGGTT <u>GATAGATGTACT</u> AATGAGCAATTGTATTAAACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC	5853
	GAGTTATATTGTGTGAGTATGTAGACT <u>TTGTTGATTCCGCTGTTAA</u> TACAATTGCT <u>ATTAGTACATCT</u> ACACCTATAAGGCTCCCCCGAT AGGAACGGCAGGCTTGGCGCGGGCTTTG	5854
	AGATGT <u>ACTAATGAGCA</u>	5855
	TGCTCATT <u>AGTACATCT</u>	5856
	TCACACAA <u>TATAACTCAGCATCATT</u> GAACAGGCATTAGCCCGTGC TTACA <u>ACTCCAATA</u> <u>ATCTTGGCTTGGAGATGGCTATGTTGAGGTT</u> CTTGC <u>GGGCCACTCAAACGCCAGGAGAATC</u>	5857
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT	GATTCTCTGGCG <u>TTTGAGTGGCCGCAAGAACCTAACATAGCCA</u> TCTCAA <u>AGCCAAGGATTATTGGAGTTGTAAGCACGGGCTAAATGC</u> CTGTT <u>CAATGATGCTGAGTTATATTGTGTGA</u>	5858
	CTCCA <u>ATAATCTTGGCT</u>	5859
	AGCCA <u>AGGATTATTGGAG</u>	5860
	TCACACAA <u>TATAACTCAGCATCATT</u> GAACAGGCATTAGCCCGTGC TTACA <u>ACTCCAATA</u> <u>ACCTTGGCTTGGAGATGGCTATGTTGAGGTT</u> CTTGC <u>GGGCCACTCAAACGCCAGGAGAATC</u>	5861
	GATTCTCTGGCG <u>TTTGAGTGGCCGCAAGAACCTAACATAGCCA</u> TCTCAA <u>AGCCAAGGTTATTGGAGTTGTAAGCACGGGCTAAATGC</u> CTGTT <u>CAATGATGCTGAGTTATATTGTGTGA</u>	5862
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAC	CTCCA <u>ATAACCTTGGCT</u>	5863
	AGCCA <u>AGGTTATTGGAG</u>	5864

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Asn100Lys AAT-AAA	GTTTGAGAGAAGAAAGGTAGACCCGAAAATGTGGCTGCAATCAT TCTAGGAGGGAGGCAA <u>AGGAGCTAA</u> ACTCTTCCCTCTTACAATGAG AGCCGCAACACCACTGTAAATATTCTCATCTT	5865
	AAGATGAATATTACAGCTGGTGGCGGCTCTCATTGTAAGAGG GAAGAGTTAGCTCC <u>TTGCCTCCTCTAGAATGATTG</u> CAGGCCAC ATTTGCGGGTCTACCTTCTCTCAAAC	5866
	GGAGGCAA <u>AGGAGCTAA</u>	5867
	TTAGCTCC <u>TTGCCTCC</u>	5868
10 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro128Leu CCG-CTG	CTTGTGCTCAAATTATGTAGGTTCTGTTGGATGCTACAG GCTGATCGATATCC <u>GATGAGTA</u> ACTGTATTAACAGCTGCATCAAC AAGATATTGTGCTGACACAGTTCAACTC	5869
	GAGTTGA <u>ACTGTGTCAGCACA</u> ATATCTTGTGATGCAGCTGTTAA TACAGTTACTCAT <u>CAGGATATCGATCAGCCTG</u> TAGCATCCACCAA CAGGAACCTAACATAATTGAAGACACAAG	5870
	CGATATCC <u>GATGAGTA</u>	5871
	TACTCAT <u>CAGGATATCG</u>	5872
	TGACACAGTTCAACTCAGCTCCCTTAATCGACATTAGCACGAAC TTATTTGGGA <u>ATAA</u> ACTTTGGAGGTGGTTCTAGAGGTA CAAACACTATGACAATAAACTCTCAGC	5873
15 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAT	GCTGAGAGTTATTATGT <u>CATAGTGT</u> TTGTACCTCTACGAAACCAC CTCCAAAGTT <u>ATATT</u> CCAAAATAAGTT <u>CGTGT</u> CTAAATGTG ATTAAGGGAA <u>AGCTGAGTTGA</u> ACTGTGTCA	5874
	TGGGA <u>ATAA</u> ACTAA <u>ACT</u>	5875
	AGTTT <u>ATATT</u> CCCA	5876
	TGACACAGTTCAACTCAGCTCCCTTAATCGACATTAGCACGAAC TTATTTGGGA <u>ATAA</u> ACTTTGGAGGTGGTTCTAGAGGTA CAAACACTATGACAATAAACTCTCAGC	5877
20 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAC	GCTGAGAGTTATTATGT <u>CATAGTGT</u> TTGTACCTCTACGAAACCAC CTCCAAAGTT <u>ATGT</u> TTCCAAAATAAGTT <u>CGTGT</u> CTAAATGTG ATTAAGGGAA <u>AGCTGAGTTGA</u> ACTGTGTCA	5878
	TGGGA <u>ATAA</u> ACTAA <u>ACT</u>	5879
	AGTTT <u>ATGT</u> TTCCCA	5880
	TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCA TTCTAGGTGGTGGT <u>AAAGGA</u> ACTCGTCTTTCCCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCCATTGGTGG	5881
25 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Val94Lys GTT-AAA	CCACCAATAGGAACAGCTGGTTAGCTCTGCTTGTAAAGAGGA AAAAGACGAGTT <u>CCCTT</u> ACCAACCTAGAATGACAGAGGGCAACA GCTTTGGATCTGCCGTGGTTCTCAA	5882
	TGGTGGT <u>AAAGGA</u> ACTC	5883

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTCCTTTACCA	5884
Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAACCAAGCTGTTCTATTGGTGGTGTACCGGCTAATTGATGTACA <u>AAATGAGTA</u> CTGCATTAACAGTGGCATACGGAAAATTTCATCTAACACAGTTCAATT	5885
	GAATTGAACGTGTTAAGATGAAAATTTCCGTATGCCACTGTTAA TGCAGTTACTCATT <u>GT</u> ACATCAATTAGCCGTAACAACCACCAATAGGAACAGCTGGTTAGCTCTGCTT	5886
	TGATGTACA <u>AAATGAGTA</u>	5887
	TACTCATT <u>GT</u> ACATCA	5888
	CACAGTTCAATTCTTTCCCTCAATCGTCACCTGCCCGCACGTA TAATTTGGAAATA <u>ATGTGGGTTTGGAGATGGATTGTGGAGGTT</u> TTAGCTGCAACCCAGACTCCAGGGGATGC	5889
Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAT	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCAC <u>ATT</u> TTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	5890
	TGGAAATA <u>ATGTGGGTT</u>	5891
	AACCCAC <u>ATT</u> TTCCA	5892
	CACAGTTCAATTCTTTCCCTCAATCGTCACCTGCCCGCACGTA TAATTTGGAAATA <u>ACGTGGGTTTGGAGATGGATTGTGGAGGTT</u> TTAGCTGCAACCCAGACTCCAGGGGATGC	5893
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCAC <u>GT</u> TTTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	5894
Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAC	TGGAAATA <u>ACGTGGGTT</u>	5895
	AACCCAC <u>GT</u> TTTTCCA	5896
	ACGTAGATTGGAAAAAGAGACCCAAGTACAGTTGTAGCAATTAT ACTAGGGTGGAGGTAA <u>AGGA</u> CTCGTCTTCCCTCACCAGC GACGAGCCAAGCCTGCTGTTCCAATTGGAGG	5897
	CCTCCAATTGGAACAGCAGGCTGGCTCGCGCTGGTGAGAGG GAAGAGACGAGTCC <u>TT</u> ACCTCCACCTAGTATAATTGCTACA GTACTGGGTCTTTTTCCAATCTACGT	5898
	TGGAGGTAA <u>AGGA</u> ACTC	5899
Increased Starch ADPGPP <i>Cicer arietinum</i> Ala101Lys GCT-AAA	GAGTCCTTTACCTCCA	5900

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP <i>Cicer arietinum</i> Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA GGCTGATAGATGTACTAATGAGTAAC TGCAATAGTGGGATCAA CAAAGTATACATTCTCACTCAATTAAATTC	5901
	GAATTAAATTGAGTGAGAATGTATACTTTGTTGATCCCACATTGAT GCAGTTACTCATTAGTACATCTATCAGCCTATAAGCACCTCCAATT GGAACACAGCAGGCTTGGCTCGCTGTTGG	5902
	AGATGTACTAATGAGTA	5903
	TACTCATTAGTACATCT	5904
Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAT	CTCAATTAAATTAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAAC TCTGGTACTAATGTCAC TTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAAC TCCAGGGGAGCA	5905
	TGCTCCCTGGAGTTGAGTTGCTGCAAGAACCTAACATAGCCA TCTCCAAAAGTGACATTAGTACCA GAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	5906
	TGGTACTAATGTCACTT	5907
	AAGTGACATTAGTACCA	5908
	CTCAATTAAATTAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAAC TCTGGTACTAACGTCACTTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAAC TCCAGGGGAGCA	5909
Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAC	TGCTCCCTGGAGTTGAGTTGCTGCAAGAACCTAACATAGCCA TCTCCAAAAGTGACGTTAGTACCA GAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	5910
	TGGTACTAACGTCACTT	5911
	AAGTGACGTTAGTACCA	5912
	ATATTGGAGAGGCCGTCGGCAAACCCCTAACAGAACATGTTGCTGCAATC ATACTGCCAGGCCGTAAAGGGACACACCTATTCCCTCACCAC CGAGCTGCAACCCCTGCTGTTCCACTTGGAG	5913
Increased Starch ADPGPP <i>Ipomoea batatas</i> Ala94Lys GCA-AAA	CTCCAAGTGGAACAGCAGGGTTGCAGCTCGATTGGTGAGAGGG AATAGGTGTGTCCTTACCGCCTGGCAGTATGATTGAGCCACA TTCTTAGGGTTGCCGACGCCCTCCAATAT	5914
	CAGGCCGTAAAGGGACA	5915
	TGTCCCTTACCGCCTG	5916
	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATA GGTTGATCGACATTCTAACATGAGCAACTGCATCAACAGCGGGGTTA ACAAGATCTTGTGCTGACCCAGTTCAATT	5917
Increased Starch ADPGPP <i>Ipomoea batatas</i> Pro122Leu CCA-CTA	GAATTGAACTGGGTAGCACAAGATCTTGTAAACCCCGCTGTTG ATGCAGTTGCTCATTAGAATGTGCAACCTATAGCATCCTCAA GTGGAACAGCAGGGTTGCAGCTGATTGG	5918
	CGACATTCTAACAGCA	5919

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TGCTCATTAGAATGTCG	5920
5 Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAT	TGACCCAGTTCAATTCAAGCTTCTCTTAACCGTCACATTCCCGTAC CGTCTTGGCAATA <u>ATGTGAGCTTCGGAGATGGATTGTTGAGGT</u> GCTGGCTGCAACCCAAACACAAGGGAAAC	5921
	GTTCCTTGTGTTGGGTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>ATTATTGCCAAAGACGGTACGGGAAATGTGA</u>	5922
	CGGTTAAGAGAAGCTGAATTGAACGGTCA	5923
	AGCTCACATTATTGCCA	5924
10 Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAC	TGACCCAGTTCAATTCAAGCTTCTCTTAACCGTCACATTCCCGTAC CGTCTTGGCAATA <u>ACGTGAGCTTCGGAGATGGATTGTTGAGGT</u> GCTGGCTGCAACCCAAACACAAGGGAAAC	5925
	GTTCCTTGTGTTGGGTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>GTTATTGCCAAAGACGGTACGGGAAATGTGA</u>	5926
	TGGCAATA <u>ACGTGAGCT</u>	5927
	AGCTCAC <u>GTTATTGCCA</u>	5928
	CATTCCGGAGGAAC <u>TTGCGGATCCAATGAGGTTGCTGCTTTA</u> TATTGGGTGGTGGCA <u>AAAGGGACTCAACTTTTCCTCTCACAAAGCA</u> CAAGGGCCACGCCTGCTGTTCTATTGGAGG	5929
15 Increased Starch ADPGPP <i>Oryza sativa</i> Thr96Lys ACC-AAA	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTGAGAGG AAAAAGTTGAGTCCC <u>TTGCCACCAACCAATATAACAGCAGCAAC</u> CTCATTGGATCCGCAAAGTTCCTCCGGAATG	5930
	TGGTGGCA <u>AAAGGGACTC</u>	5931
	GAGTCCC <u>TTGCCACCA</u>	5932
	CAAGCACAAGGGCCACGCCTGCTGTTCTATTGGAGGATGCTATA GGCTTATCGATAT <u>CCCATGAGCAACTGTTCAACAGTGGCATAAA</u> CAAGATATTCTATA <u>ATGACTCAATTCAACTC</u>	5933
	GAGTTGAATTGAGTCATTATGAATATCTTGT <u>TTATGCCACTGTTGAA</u> ACAGTTGCTCAT <u>GAGGATATCGATAAGCCTATAGCATCCTCCAATA</u> GGAACAGCAGGCGTGGCCCTTGTGCTTG	5934
20 Increased Starch ADPGPP <i>Oryza sativa</i> Pro124Leu CCC-CTC	CGATAT <u>CCCATGAGCA</u>	5935
	TGCTCAT <u>GAGGATATCG</u>	5936
	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCACTCGTAC GTACCTTGGTGG <u>TAATATCAACTTTACTGATGGTTCTGTTGAGGTA</u> TTAGCCGCTACACAAATGCCTGGGGAGGC	5937
	GCCTCCCCAGGCATTGTGAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT <u>ATTACCAACCAAGGTACGTACGATGAATGTGAC</u> GATTAAGAGATGCTGAGTTGAATTGAGTC	5938
25 Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TGGTGGTAATATCAACT	5939
	AGTTGATATTACCACCA	5940
Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCACTGTAC GTACCTTGGTGGTAACATCAACTTACTGATGGTCTGTTGAGGTA TTAGCCGCTACACAAATGCCCTGGGGAGGC GCCTCCCCAGGCATTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGATGTTACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA TGGTGGTAACATCAACT	5941 5942 5943
	AGTTGATGTTACCACCA	5944
Increased Starch ADPGPP <i>Triticum aestivum</i> Thr80Lys ACC-AAA	GTCCCTCAGGAGGATTAAGCGATCCGAACCGAGGTGCGGCCGTC ATACTCGCGGGCGCAAAGGGACTCAGCTCTCCCACTCACGAG CACAAGGGCCACACCTGCTGTTCTATTGGAGG CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTAGTGG GAAGAGCTGAGTCCCTTGC CGCCGAGTATGACGGCCGCAA CCTCGTTGGATCGCTTAATCCTCCTGAAGGAC CGCGGCCAAAGGGACTC GAGTCCCCTTGC CGCCG	5945 5946 5947 5948
Increased Starch ADPGPP <i>Triticum aestivum</i> Pro108Leu CCC-CTC	CGAGCACAAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGACATTCTCATGAGCAACTGCTTCAACAGTGGCATCA ACAAGATATTGTCATGACCCAGTTCAACTC GAGTTGAACTGGGTATGACGAATATCTTGTGATGCCACTGTTG AAGCAGTTGCTCATGAGAATGTCATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGCTCG CGACATTCTCATGAGCA TGCTCATGAGAATGTCG	5949 5950 5951 5952
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCCTCCCTTAATCGTCACATTACCGCA CCTACCTCGCGGGAAATATCAATTCACTGATGGATCCGTTGAGG TATTGGCCCGACGCAAATGCCGGGGAGGC GCCTCCCCGGCATTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAATTGATATTCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACCTGGTCA CGCGGGAAATATCAATT AATTGATATTCCCGCCG	5953 5954 5955 5956
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCCTCCCTTAATCGTCACATTACCGCA CCTACCTCGCGGGAAACATCAATTCACTGATGGATCCGTTGAGG TATTGGCCCGACGCAAATGCCGGGGAGGC	5957

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCCTCCCCGGCATTGCGTCGCCAACACCTAACGGATCC ATCAGTGAATTGAT <u>GTT</u> CCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACGGTCA	5958
	CGGCGGG <u>AAC</u> ATCAATT	5959
	AATTGAT <u>GTT</u> CCGCCG	5960
5 Increased Starch ADPGPP <i>Oryza sativa</i> Thr95Lys ACT-AAA	CCTCCCAGAAAGAATTATGCTGATGCAAGCCACGTTCTGCTGTCA TTTGGGTGGAGGCA <u>AAGGAG</u> TTCAACTCTTCCTCTGACAAGCA CAAGGGCTACCCCCGCTGTTCTGTTGGAGG	5961
	CCTCCAACAGGAACAGCAGGGGGTAGCCCTGTGCTTGTAGAGG AAAGAGTTGA <u>ACTCC</u> TTGCCTCCACCCAAAATGACAGCAGAAC GTGGCTTGATCAGCATAATTCTTCGGGAGG	5962
	TGGAGG <u>CAAAGGAG</u> TTCA	5963
	GA <u>ACTCC</u> TTGCCTCCA	5964
	CAAGCACAAGGGCTACCCCCGCTGTTCTGTTGGAGGATGTTACA GGCTTATTGACAT <u>CC</u> TTATGAGCAATTGCTCAATAGCGGAATAAA TAAAATATTGTGATGACTCAGTTCAATT	5965
10 Increased Starch ADPGPP <i>Oryza sativa</i> Pro123Leu CCT-CTT	GAATTGA <u>ACTGAGTC</u> ATCACAATATTATTATTCCGCTATTGAA GCAATTGCTCATA <u>AGGATGT</u> CAATAAGCCTGTAACATCCTCCAACA GGAACACAGCAGGGGGTAGCCCTGTGCTTG	5966
	TGACAT <u>CC</u> TTATGAGCA	5967
	TGCTCATA <u>AGGATGT</u> CA	5968
	TGACTCAGTTCAATTCTGCTTCTCTTAATGCCATATCCATCATAAC ATACCTGGTGG <u>AAAT</u> ATCAACTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCGTGACGAACC	5969
	GGTTCGTCA <u>GGC</u> ATTGTGAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT <u>AT</u> CCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGA <u>ACTGAGT</u> CA	5970
15 Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAT	TGGTGG <u>GAAT</u> ATCAACT	5971
	AGTTGAT <u>AT</u> CCACCA	5972
	TGACTCAGTTCAATTCTGCTTCTCTTAATGCCATATCCATCATAAC ATACCTGGTGG <u>AAAC</u> ATCAACTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCGTGACGAACC	5973
	GGTTCGTCA <u>GGC</u> ATTGTGAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT <u>GTT</u> CCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGA <u>ACTGAGT</u> CA	5974
	TGGTGG <u>GAAC</u> ATCAACT	5975
20 Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAC	AGTTGAT <u>GTT</u> CCACCA	5976

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased Starch ADPGPP <i>Triticum aestivum</i> Thr99Lys ACC-AAA	CCTTCCGCAGGAATTACGCCGATCCGAACGAGGTGCGGCCGTC ATACTCGGCGGTGGCAAAGGGACTCAGCTTCCCTCTCACAAG CACAGGGCCACACCTGCTGTTCCATTGGAGG	5977
	CCTCCAATAGGAACAGCAGGTGTGCCCTTGTGCTGTGAGAGG GAAGAGCTGAGTCCC <del>TT</del> GCCACGCCGAGATATGACGCCGCGA CCTCGTTCGGATCGCGTAATTCCCTGCGGAAGG	5978
	CGGTGGCAAAGGGACTC	5979
	GAGTCCCT <del>TT</del> GCCACCG	5980
10 Increased Starch ADPGPP <i>Triticum aestivum</i> Pro127Leu CCC-CTC	CAAGCACAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGATATT <del>TC</del> CATGAGCAACTGCTCAATAGTGGCATCAA CAAGATATTCGTCATGACGCCAGTTCAACTC	5981
	GAGTTGA <del>CT</del> GCGTCATGACGAATATCTTGTGATGCCACTATTGA AGCAGTTGCTCATG <del>AGA</del> ATATCGATGAGCCTGTAACATCCTCAA TAGGAACAGCAGGTGTGCCCTTGTGCTG	5982
	CGATATT <del>TC</del> CATGAGCA	5983
	TGCTCATGAGAATATCG	5984
15 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAT	TGACGCAGTTCAACTCGGCCCTCTTAATCGTCACATTACCGCA CCTACCTCGGCGGGAA <del>AT</del> ATCAATTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCGGGGAGGC	5985
	GCCTCCCCGGGCATTGCGTCGCCAATACCTCAACAGATCC ATCAGTGA <del>AA</del> ATTGAT <del>AT</del> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGA <del>CT</del> GCGTCA	5986
	CGGC <del>GGG</del> AA <del>AT</del> ATCAATT	5987
	AATTGAT <del>AT</del> CCCGCCG	5988
20 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAC	TGACGCAGTTCAACTCGGCCCTCTTAATCGTCACATTACCGCA CCTACCTCGGCGGGAA <del>AC</del> ATCAATTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCGGGGAGGC	5989
	GCCTCCCCGGGCATTGCGTCGCCAATACCTCAACAGATCC ATCAGTGA <del>AA</del> ATTGAT <del>GT</del> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGA <del>CT</del> GCGTCA	5990
	CGGC <del>GGG</del> AA <del>AC</del> ATCAATT	5991
	AATTGAT <del>GT</del> CCCGCCG	5992
25 Increased Starch ADPGPP <i>Zea mays</i> Thr96Lys ACC-AAA	CTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA TTTGGGTGGTGGTAAAGGGACTCAGCTTCCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCCATTGGAGG	5993
	CCTCCAATAGGAACAGCAGGGGTGCCCTTGTGCTGTGAGAGG GAAAAGCTGAGTCCC <del>TT</del> ACCACCA <del>CC</del> AAATGACGCCAGCGAC TTCATTAGGATCAGCATAATTCCCTCCGAAAG	5994
	TGGTGGTAAAGGGACTC	5995

Phenotype: Gene Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GAGTCCC <u>T</u> ACCA	5996
Increased Starch ADPGPP Zea mays Pro124Leu CCC-CTC	CAAGCACAAGGGCCACCCCTGCTGTTCTATTGGAGGATGTTACA GGCTTATTGATATCC <u>T</u> CATGAGCACTGTTCAACAGTGGCATAAA CAAGATATTGTTATGACTCAGTTCAACTC	5997
	GAGTTGA <u>ACT</u> GAGTCATAACAAATATCTGTTATGCCACTGTTGA AACAGTTGCTCATG <u>AGG</u> ATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGTGGCCCTGTGCTTG	5998
	TGATATCC <u>T</u> CATGAGCA	5999
	TGCTCATG <u>AGG</u> ATATCA	6000
Increased Starch ADPGPP Zea mays Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCACTGTAC CTATCTTGGTGG <u>GA</u> ATATCAACTTC <u>ACT</u> GATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCC <u>T</u> GGGGAGGC	6001
	GCCTCCCCAGGC <u>ATT</u> GTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGAT <u>ATT</u> CCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGA <u>ACT</u> GAGTC	6002
	TGGTGG <u>GA</u> ATATCAACT	6003
	AGTTGAT <u>ATT</u> CCCACCA	6004
Increased Starch ADPGPP Zea mays Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCACTGTAC CTATCTTGGTGG <u>GA</u> ACATCAACTTC <u>ACT</u> GATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCC <u>T</u> GGGGAGGC	6005
	GCCTCCCCAGGC <u>ATT</u> GTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGAT <u>GT</u> CCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGA <u>ACT</u> GAGTC	6006
	TGGTGG <u>GA</u> ACATCAACT	6007
	AGTTGAT <u>GT</u> CCCACCA	6008
Increased Starch ADPGPP <i>Solanum tuberosum</i> Ala58Lys GCG-AAG	CTTGAGAGGCAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGG <u>AA</u> AGGGAA <u>CT</u> CGTCTTCCCCTCACCAA ACGTCGTGCTAAGCCTGCCGTTCC <u>A</u> GGGAG	6009
	CTCCCATTGGAACGGCAGGCTTAGCACGACGTTGGTGAGGGGG AAAAGACGAGTTCC <u>T</u> TTCCCCTCTAGAATGATTGCTACTACTG TCCTTG <u>C</u> ATGCC <u>CT</u> TTTG <u>C</u> CTCAAG	6010
	GAGGGGG <u>AA</u> AGGGAA <u>CT</u>	6011
	AGTTCCC <u>T</u> TTCCCCTC	6012
Increased Starch ADPGPP <i>Solanum tuberosum</i> Pro86Leu CCA-CTA	CCAAACGTCGTGCTAAGCCTGCCGTTCC <u>A</u> GGGAGGAGCATATA GGCTAATTGATGT <u>A</u> CTAATGAGCA <u>CT</u> GTATTAA <u>AC</u> AGTGGCATCAA CAAAGTATACATTCTCACTCAATTCAACTC	6013
	GAGTTGAATTGAGTGAGAATGTATA <u>CT</u> TTGTTGATGCC <u>ACT</u> GTTAA TACAGTTGCTCAT <u>AG</u> TACATCAATTAGCCTATATGCTCCTCCC <u>A</u> TGGAACGGCAGGCTAGCACGACGTTGG	6014

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATGTACTAATGAGCA	6015
	TGCTCATTAGTACATCA	6016
Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAT	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAATAATGTCACATTGAGAGTGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6017
	AATTCACCTGGTGTGAGTTGCTGCTAACGACCTCGACATAGCCA CTCTCGAATGTGACATTATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	6018
	TGGCAATAATGTCACAT	6019
	ATGTGACATTATTGCCA	6020
Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAC	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAATAACGTCACATTGAGAGTGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6021
	AATTCACCTGGTGTGAGTTGCTGCTAACGACCTCGACATAGCCA CTCTCGAATGTGACGTTATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	6022
	TGGCAATAACGTCACAT	6023
	ATGTGACGTTATTGCCA	6024
Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAA	TATTGAATCTCCAAAAGCTGACCCAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAAAGGGACTCGCCTCTTCCTCTTACTAGCA GGAGAGCTAACGCCAGCAGTGCCAATTGGAGG	6025
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCCCTTACCAACCACCCAGCACAATTGCAGGCCACA TTTTGGGTAGCTTTGGAGATTCAAATA	6026
	TGGTGGTAAAGGGACTC	6027
	GAGTCCCCTTACCAACCA	6028
Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAC	TATTGAATCTCCAAAAGCTGACCCAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAAACGGGACTCGCCTCTTCCTCTTACTAGCA GGAGAGCTAACGCCAGCAGTGCCAATTGGAGG	6029
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCCCTTACCAACCACCCAGCACAATTGCAGGCCAC TTTTGGGTAGCTTTGGAGATTCAAATA	6030
	TGGTGGTAAACGGGACTC	6031
	GAGTCCCCTTACCAACCA	6032
Increased Starch ADPGPP <i>Beta vulgaris</i>	CTAGCAGGAGAGCTAACGCCAGCAGTGCCAATTGGAGGGTGTAC AGGCTGATTGATGTGCTATGAGCAACTGCATCACACAGTGGCATT AGAAAGATTTCATTCTACCCAGTTCAATT	6033

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Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEG ID NO:
	GAATTGAAC TGGGTAAGAATGAAAATCTTCTAATGCCACTGTTGA TGCAGTTGCTCATA <u>AG</u> CACATCAATCAGCCTGTAACACCCCTCCAA TTGGCACTGCTGGCTTAGCTCTCCTGCTAG	6034
	TGATGTGCT <u>T</u> ATGAGCA	6035
	TGCTCATA <u>AG</u> CACATCA	6036
5 Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAT	CCCAGTTCAATTGTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTGGAGATA <u>AAT</u> GTGAATTTGGGGATGGCTTGAGGTT TTTGCTGCTACACAAACACCTGGAGAAC	6037
	GATTCTCCAGGTGTTGTGTAGCAGCAAAACCTCCACAAAGCCA TCCCCAAAATT <u>CAC</u> ATTATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAAC TGGG	6038
	TGGAGATA <u>AAT</u> GTGAATT	6039
	AATT <u>CAC</u> ATTATCTCCA	6040
	CCCAGTTCAATTGTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTGGAGATA <u>AC</u> GTGAATTTGGGGATGGCTTGAGGTT TTTGCTGCTACACAAACACCTGGAGAAC	6041
10 Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAC	GATTCTCCAGGTGTTGTGTAGCAGCAAAACCTCCACAAAGCCA TCCCCAAAATT <u>CAC</u> GT <u>T</u> ATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAAC TGGG	6042
	TGGAGATA <u>AC</u> GTGAATT	6043
	AATT <u>CAC</u> GT <u>T</u> ATCTCCA	6044

**Table 21**  
**Oligonucleotides to produce plants with waxy starch**

5	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
10	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTTCATATGGCAACTGTGACTGCTTC TTCTAACTTGTGT <u>GAAGAAC</u> TTCAACAAATCATGGTGCTT CTTCATGCTCTGATGTCGCTCAGATTAC	6045
		GTAATCTGAGCGACATCAGAGCATGAAGAACCATGATTGTTGA AAAGTGAAGTTCTT <u>CACACAAAG</u> TTAGAAGAACAGTCACAGTTGC CATTATGAAC <del>T</del> ACCCGTTACCTGGATT	6046
		CTTGTGT <u>GAAGAAC</u> TT	6047
		AAGTTCTT <u>CACACAAAG</u>	6048
15	Waxy starch GBSS <i>Arabidopsis thaliana</i> Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTTCATATGGCAACTGTGACTGCTTCTT CTAACTTGTGT <u>CAT</u> <u>GAAC</u> TTCAACAAATCATGGTGCTTCT TCATGCTCTGATGTCGCTCAGATTACCT	6049
		AGGTAATCTGAGCGACATCAGAGCATGAAGAACCATGATTGTT GAAAAGTGAAGTT <u>CAT</u> <u>GACACAAAG</u> TTAGAAGAACAGTCACAGTT GCCATTATGAAC <del>T</del> ACCCGTTACCTGGAT	6050
		TTGTGT <u>CAT</u> <u>GAAC</u> TTCA	6051
		TGAAGTT <u>CAT</u> <u>GACACAA</u>	6052
		TAAACGGGTAGTTCATATGGCAACTGTGACTGCTTCTTCAACTT TGTGT <u>CAAGAAC</u> TT <u>GACT</u> TTCAACAAATCATGGTGCTTCTTCATGCT CTGATGTCGCTCAGATTACCTAAAAGG	6053
20	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	CCTTTAAGGTAA <u>CTGAGCGACATCAGAGCATGAAGAAC</u> CCAT GATTGTTGAAAAGT <u>CAAGTTCTGACACAAAG</u> TTAGAAGAACAGT CACAGTTGCCATTATGAAC <del>T</del> ACCCGTTA	6054
		AAGAAC <u>TTGACT</u> TTCA	6055
		TGAAAAGT <u>CAAGTTCTT</u>	6056
		TGACTGCTCTTCAACTTGTGT <u>CAAGAAC</u> TTCAACAAAT CATGGTGCTTCTT <u>GATGCTCTGATGTCGCTCAGATTACCTAAAAG</u> GCCAATCCTTGACTCATTGTGGGTTAAG	6057
25	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser24Term TCA-TGA	CTTAACCCACAAT <u>GAGTCAGGATTGGCCTTTAAGG</u> TAATCTGAG CGACATCAGAGCAT <u>CAAGAAC</u> CCATGATTGTTGAAAAGTGAAGT TCTTGACACAAAGTTAGAAGAACAGTC	6058
		TGCTTCTT <u>GATGCTCTG</u>	6059
		CAGAGCAT <u>CAAGAAC</u> CA	6060

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Arabidopsis thaliana</i> Cys25Term TGC-TGA	TGCTTCTTCTAACCTTGTGTCAAGAACCTCACTTTCAACAATCATG GTGCTTCTTCATG <u>A</u> CTGATGTCGCTCAGATTACCTAAAAGGCCA ATCCTTGACTCATGTGGGTTAAGGTCA	6061
		TGACCTTAACCCACAATGAGTCAGGATTGGCCTTTAAGGTAATC TGAGCGACATCAG <u>A</u> CATGAAGAAGCACCATGATTGTTGAAAAGTG AAGTTCTGACACAAAGTTAGAAGAAGCA	6062
		TCTTCATG <u>A</u> CTGATGT	6063
		ACATCAG <u>A</u> CATGAAGA	6064
10	Waxy starch GBSS <i>Antirrhinum majus</i> Lys24Term AAA-TAA	GTAACAGCTTCACAGTTGGTGTACATGTCCATGGTGGAGCAACG TCTTCACCGGATACT <u>A</u> AAACAAACTTGGCCCAGGTTGGCCTCAGG AACCAAGCAATTCACTCACAATGGGTTGAGAT	6065
		ATCTCAACCCATTGTGAGTGAATTGCTGGTCTGAGGCCAACCT GGGCCAAGTTGTT <u>A</u> AGTATCCGGTGAAGACGTTGCTCCACCAT GGACATGTGACACCAACTGTGAAGCTGTTAC	6066
		CGGATACT <u>A</u> AAACAAAC	6067
		GT <u>TT</u> GTT <u>A</u> AGTATCCG	6068
		CACAGTTGGTGTACATGTCCATGGTGGAGCAACGTCTCACCGG ATACTAAACAAACT <u>A</u> GGCCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAATGGGTTGAGATCAATAAACAT	6069
15	Waxy starch GBSS <i>Antirrhinum majus</i> Leu27Term TTG-TAG	ATGTTTATTGATCTAACCCATTGTGAGTGAATTGCTGGTCTGA GGCCAACCTGGGCC <u>T</u> AGTTGTTAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG	6070
		AACAAACT <u>A</u> GGCCCAGG	6071
		CCTGGGCC <u>T</u> AGTTGTT	6072
		TTGGTGTACATGTCCATGGTGGAGCAACGTCTCACCGGATACT AAAACAAACTTGGCCT <u>T</u> AGGTTGGCCTCAGGAACCAGCAATTCACT CACAATGGGTTGAGATCAATAAACATGGTTG	6073
		CAACCATGTTATTGATCTAACCCATTGTGAGTGAATTGCTGGTT CCTGAGGCCAACCT <u>A</u> GGCCAAGTTGTTAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA	6074
20	Waxy starch GBSS <i>Antirrhinum majus</i> Gln29Term CAG-TAG	ACTTGGCC <u>T</u> AGGTTGGC	6075
		GCCAACCT <u>A</u> GGCCAAGT	6076
		GGTGGAGCAACGTCTCACCGGATACTAAAACAAACTTGGCCCAG GTTGGCCTCAGGAAC <u>T</u> AGCAATTCACTCACAATGGGTTGAGATCAA TAAACATGGTTGATAAGCTTCAAATGAGGA	6077
		TCCTCATTTGAAGCTTATCAACCATGTTATTGATCTCAACCCATTG TGAGTGAATTGCT <u>A</u> GTTCTGAGGCCAACCTGGGCCAAGTTGTT TTAGTATCCGGTGAAGACGTTGCTCCACC	6078

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCAGGAAC <u>T</u> AGCAATT	6079
	GAATTGCT <u>A</u> TTCCCTGA	6080
5 Waxy starch GBSS <i>Antirrhinum majus</i> Gln36Term CAA-TAA	GGAGCAACGTCTCACCGGATACTAAAACAAACTGGGCCAGGTT GGCCTCAGGAACCAG <u>T</u> AATTCACTCACAATGGGTTGAGATCAATAA ACATGGTTGATAAGCTTCAAATGAGGAACA	6081
	TGTTCCCTCATTTGAAGCTTATCAACCATGTTATTGATCTCAACCCA TTGTGAGTGAATTACTGGTTCTGAGGCCAACCTGGGCCAAGTTT GTTTAGTATCCGGTGAAGACGTTGCTCC	6082
	GGAACCAG <u>T</u> AATTCACT	6083
	AGTGAATT <u>A</u> CTGGTTCC	6084
10 Waxy starch GBSS <i>Ipomoea batatas</i> Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTGTTCATGTCTGTG GGGGTGCCACTTCT <u>T</u> GAGAATCAAAGTGGGGTTGGGTCATTAG CCCTGAGGAGCCAAGCTGTGACTCACAATG	6085
	CATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACC CCACTTTGATTCT <u>A</u> AGAAGTGGCACCCCCACAGACATGAGAAA CAAAGTGTGAGGCAGTTAGTCGCCATCAC	6086
	CCACTTCT <u>T</u> GAGAATCA	6087
	TGATTCT <u>A</u> AGAAGTGG	6088
15 Waxy starch GBSS <i>Ipomoea batatas</i> Glu21Term GAA-TAA	ATGGCGACTATAACTGCCTCACACTTGTTCATGTCTGTGGGG GTGCCACTCTGG <u>A</u> ATCAAAGTGGGGTTGGGTCATTAGCCC TGAGGAGCCAAGCTGTGACTCACAATGGGT	6089
	ACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCA ACCCCAC <u>T</u> TTGATT <u>A</u> CCAGAAGTGGCACCCCCACAGACATGAG AAACAAAGTGTGAGGCAGTTAGTCGCCAT	6090
	CTTCTGG <u>A</u> ATCAAA	6091
	TTTGATT <u>A</u> CCAGAAG	6092
20 Waxy starch GBSS <i>Ipomoea batatas</i> Ser22Term TCA-TGA	CGACTATAACTGCCTCACACTTGTTCATGTCTGTGGGGTGC CACTTCTGGAGAAT <u>G</u> AAAAGTGGGGTTGGGTCATTAGCCCCTGAG GAGCCAAGCTGTGACTCACAATGGGTGAG	6093
	CTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGA CCCAACCCACTTT <u>C</u> ATTCTCCAGAAGTGGCACCCCCACAGACA TGAGAAACAAAGTGTGAGGCAGTTAGTCG	6094
	TGGAGAAT <u>G</u> AAAAGTGG	6095
	CCACTTT <u>C</u> ATTCTCCA	6096

Phenotype, Gene, Plant & Targeted Alteration		Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Ipomoea batatas</i> Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTGTTCATGTCCTGTGGGGTGCCT CTTCTGGAGAATCAT <u>A</u> AGTGGGGTGGTCATTAGCCCTGAGGA GCCAAGCTGTGACTCACAATGGGTTGAGAC	6097
		GTCTCAACCCATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATT GACCCAACCCCCACT <u>T</u> ATGATTCTCCAGAAGTGGCACCCCCACAGA CATGAGAAACAAAGTGTGAGGCAGTTAGT	6098
		GAGAATCAT <u>A</u> AGTGGGG	6099
		CCCCACTT <u>T</u> ATGATTCTC	6100
10	Waxy starch GBSS <i>Ipomoea batatas</i> Leu26Term TTG-TAG	CCTCACACTTGTTCATGTCCTGTGGGGTGCCTCTGGAGA ATCAAAAGTGGGGT <u>A</u> GGGTCAATTAGCCCTGAGGAGCCAAGCTGT GACTCACAATGGGTTGAGACCTGTGAACAA	6101
		TTGTTCACAGGTCTCAACCCATTGTGAGTCACAGCTGGCTCCTCA GGGCTAATTGACC <u>T</u> ACCCCCACTTTGATTCTCCAGAAGTGGCAC CCCCACAGACATGAGAAACAAAGTGTGAGG	6102
		AGTGGGGT <u>A</u> GGGTCAAT	6103
		ATTGACC <u>T</u> ACCCCCACT	6104
		CATCGGCGATTGTTGCTCCTTACTGCTCTCACAGAACGGCAAC GGTGACGGGTCT <u>T</u> AGGTGGTGTGAGAAGCGCGTGCTCAATT CCAGGGAAAGAACAGAACGCAAAGTGAATTCA	6105
15	Waxy starch GBSS <i>Astragalus membranaeus</i> Tyr8Term TAT-TAG	TGAATTCACTTGGCTCTGTTCTCCCTGGGAATTGAAGCACGCG CTTCTCGACACCAC <u>C</u> TAAGACCCCCGTACCGTTGCCATTCTGTGA GAGAGCAGTAAGGAGCAACAATGCCGATG	6106
		GGGTCT <u>T</u> AGGTGGTGTGTC	6107
		GACACCAC <u>C</u> TAAGACCC	6108
		ATTGTTGCTCCTTACTGCTCTCACAGAACGGCAACGGTGACGG GGTCTTATGTGGGT <u>T</u> AGAGAAGCGCGTGCTCAATTCCCAGGGAA GAACAGAACGCAAAGTGAATTACCTCAGAA	6109
		TTCTGAGGTGAATTCACTTGGCTCTGTTCTCCCTGGGAATTGA AGCACCGCGTTCT <u>T</u> ACACCCACATAAGACCCCCGTACCGTTGCCA TTCTGTGAGAGAGCAGTAAGGAGCAACAAT	6110
20	Waxy starch GBSS <i>Astragalus membranaeus</i> Ser11Term TCG-TAG	TGTGGT <u>T</u> AGAGAACGCG	6111
		CGCTTCT <u>T</u> ACACCCACA	6112

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Astragalus membranaeus</i> Arg12Term AGA-TGA	TGTTGCTCCTTACTGCTCTCACAGAATGGCAACGGTGACGGGG TCTTATGTGGTGT <u>CGT</u> GAAGCGCGTCTCAATTCCCAGGGAAAGA ACAGAAGCAAAGTGAATTCACCTCAGAAGA	6113
	TCTTCTGAGGTGAATTCACTTGGCTCTGTTCTCCCTGGATT GAAGCACGCGCTTC <u>ACG</u> ACACACATAAGACCCCGTCACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA	6114
	TGGTGT <u>CGT</u> GAAGCGCG	6115
	CGCGCTT <u>ACG</u> ACACCA	6116
10 Waxy starch GBSS <i>Astragalus membranaeus</i> Cys15Term TGC-TGA	ACTGCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGT GTCGAGAAGCGCGT <u>GATT</u> CAATTCCCAGGGAAAGAACAGAACCAA AGTGAATTCACCTCAGAAGATAAAATCTCAAT	6117
	ATTGAGATTATCTTCTGAGGTGAATTCACTTGGCTCTGTTCTC CCTGGGAATT <u>GAAT</u> CACGCGCTCTCGACACACATAAGACCCCG TCACCGTTGCCATTCTGTGAGAGAGCAGT	6118
	AGCGCGT <u>GATT</u> CAATT	6119
	GAATT <u>GAAT</u> CACGCGCT	6120
15 Waxy starch GBSS <i>Astragalus membranaeus</i> Gln19Term CAG-TAG	CACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGT <u>GAGAACG</u> GCGTGCTTC <u>ATT</u> CC <u>TA</u> GGGAAGAACAGAACGCCAAAGTGAATT <u>CA</u> CCTCAGAAGATAAA <u>AT</u> CTCAATAG <u>CCAAGC</u> AT	6121
	ATGCTTGGCTATTGAGATTATCTTCTGAGGTGAATTCACTTGGCT TCTGTTCTCC <u>CTA</u> GG <u>ATT</u> GAAGCACGCGCTCTCGACACACAT AAGACCCCGTCACCGTTGCCATTCTGTG	6122
	TCAATT <u>CC</u> <u>TA</u> GGGAAGA	6123
	TCTTCC <u>CTA</u> GG <u>ATT</u> GA	6124
20 Waxy starch GBSS <i>Solanum tuberosum</i> Ser7Term TCA-TGA	TGTAGCTTGGTAGATT <u>CCC</u> <u>CTT</u> <u>TT</u> GTAGACCACACATCACATGGC AAGCATCACAGCTT <u>GACACC</u> ACTTGTGT <u>CAAGAAC</u> CCAA <u>CTT</u> CA CTAGACACCAAA <u>AT</u> CAAC <u>CTT</u> GT <u>ACAGAT</u>	6125
	ATCTGTGAC <u>AGGTGATT</u> GGTGT <u>CAAGTGAAGTTGGCT</u> CTTG ACACAA <u>AGGGTGTCAAGCTGT</u> ATGCTGCCATGTGATGTGG TCTACAAA <u>AGGGGAAT</u> CTACCAAG <u>CTACA</u>	6126
	CACAGCTT <u>GACACC</u> ACT	6127
	AGTGGTGT <u>CAAGCTGTG</u>	6128
25 Waxy starch GBSS <i>Solanum tuberosum</i> Ser12Term TCA-TGA	TCCCCTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC ACACCA <u>CTT</u> GTG <u>TAAGAAGCCAA</u> ACTTCACTAGACACCAAA <u>AT</u> CA AC <u>CTT</u> GT <u>CAAGATAGGACTCAGGAACCA</u>	6129
	TGGTT <u>CC</u> <u>CTGAGTCCTATCTGTGAC</u> AGGTGATTGGTGT <u>CAAGT</u> AAGTTGGCTT <u>CTT</u> <u>CAACAAAGTGGTGTGAAGCTGT</u> ATGCTGC CATGTGATGTGGT <u>CTACAAAAGGGGA</u>	6130

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTTTGTGT <u>GAAGAAGCC</u>	6131
	GGCTTCTT <u>CACACAAAG</u>	6132
Waxy starch GBSS <i>Solanum tuberosum</i>	CCCTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCAC ACCACTTTGTGT <u>CATGAAGC</u> AAACTCACTAGACACACCAATCAAC CTTGTACAGATAGGACTCAGGAACCATA	6133
Arg13Term AGA-TGA	TATGGTTCC <u>TGAGTC</u> CTATCTGTGACAAGGTTGATTGGTGTCTAG TGAAGTTGGCTT <u>CATGACACAAAGTGGTGTGAAGCTGTGATGCTT</u> GCCATGTGATGTGTGGTCTACAAAAAGGG	6134
	TTGTGT <u>CATGAAGC</u> CAA	6135
	TTGGCTT <u>CATGACACAA</u>	6136
Waxy starch GBSS <i>Solanum tuberosum</i>	TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACT TTGTGT <u>CAAGAAGC</u> TAACACTCACTAGACACACCAATCAACCTTGT ACAGATAGGACTCAGGAACCATACTCTGA	6137
Gln15Term CAA-TAA	TCAGAGTATGGTTCC <u>TGAGTC</u> CTATCTGTGACAAGGTTGATTGGT GTCTAGTGAAGTT <u>AGCTT</u> CTTGACACAAAGTGGTGTGAAGCTGTG ATGCTTGCCATGTGATGTGTGGTCTACAA	6138
	CAAGAAGC <u>TAAC</u> TTCA	6139
	TGAAGTT <u>AGCTT</u> CTTG	6140
Waxy starch GBSS <i>Solanum tuberosum</i>	CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTC AAGAAGC <u>AAACTT</u> <u>GACT</u> AGACACCAATCAACCTTGTACAGATA GGACTCAGGAACCATACTCTGACTCACAA	6141
Ser17Term TCA-TGA	TTGTGAGTCAGAGTATGGTTCC <u>TGAGTC</u> CTATCTGTGACAAGGTTG ATTTGGTGTCTAGT <u>CAAGTT</u> GGCTTCTTGACACAAAGTGGTGTGA AGCTGTGATGCTGCCATGTGATGTGTGG	6142
	CCAAACTT <u>GACT</u> AGACA	6143
	TGTCTAGT <u>CAAGTT</u> GG	6144
Waxy starch GBSS <i>Pisum sativum</i>	GTCGATCACTCTCTCACCGCCGAAACAGATTGACACAAAAA TGGCAACAATAACG <u>TGAT</u> CTTCAATGCCGACGAGAACCGCGTGCT TCAATTACCAAGGAAGATCAGCAGAGTCTA	6145
Gly6Term GGA-TGA	TAGACTCTGCTGATCTCCTGGTAATTGAAGCACGCCGGTCTCGT CGGCATTGAAGAT <u>CACGTT</u> ATTGTTGCCATTGTGTC GTTTCGGCGGTGAGAGAAGAGTGTGAC	6146
	CAATAACG <u>TGAT</u> CTTCA	6147
	TGAAGAT <u>CACGTT</u> ATTG	6148

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Pisum sativum</i> Ser8Term TCA-TGA	ACTCTTCTCTCACCGCCGAAACAGATTTGACACAAAAATGGCAAC AATAACGGGATCTT <u>GAATGCCGACGAGAACCGCGTGCTTCATTAA</u> CCAAGGAAGATCAGCAGAGTCTAAACTGAA	6149
		TTCAGTTAGACTCTGCTGATCTTCCTGGTAATTGAAGCACGCGG TTCTCGTCGGCATT <u>CAAGATCCC GTTATTGTTGCCATT</u> TTGTGTC AAAATCTGTTCGGGCGT GAGAGAAGAGT	6150
		GGGATCTT <u>GAATGCCGA</u>	6151
		TCGGCATT <u>CAAGATCCC</u>	6152
10	Waxy starch GBSS <i>Pisum sativum</i> Arg12Term AGA-TGA	ACCGCCGAAACAGATTTGACACAAAAATGGCAACAATAACGGGAT CTTCAATGCCGACG <u>TGAACCGCGTGCTTCATTACCAAGGAAGAT</u> CAGCAGAGTCTAAACTGAATTGCCTCAGA	6153
		TCTGAGGCAAATT <u>CAGTTAGACTCTGCTGATCTTCCTGGTAATT</u> GAAGCACCGCGGTT <u>ACGT CGGCATTGAAGATCCC GTTATTGTTGC</u> CATTTTGTTGTCAAATCTGTTCGGGCGT	6154
		TGCCGACG <u>TGAACCGCG</u>	6155
		CGCGGTT <u>ACGT CGGC</u> A	6156
		AGATTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCG ACGAGAACCGCGTG <u>ATTCAATTACCAAGGAAGATCAGCAGAGTCT</u> AAACTGAATTGCCTCAGATA <u>CACTTCAT</u>	6157
15	Waxy starch GBSS <i>Pisum sativum</i> Cys15Term TGC-TGA	ATTGAAGTGTATCTGAGGCAAATT <u>CAGTTAGACTCTGCTGATCTT</u> CCTTGGTAATT <u>GAATCACGCGGTTCTCGTCGGCATTGAAGATCCC</u> GTTATTGTTGCCATT <u>TTGTGTCAAATCT</u>	6158
		ACCGCGT <u>GATTCAATT</u>	6159
		TAATT <u>GAATCACGCGG</u> T	6160
		CACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAAC CGCGTGCTTCAATT <u>AGCAAGGAAGATCAGCAGAGTCTAAACTGAAT</u> TTGCCCTCAGATA <u>CACTTCATAACAACCAA</u>	6161
		TTGGTTGTTATT <u>GAAGTGTATCTGAGGCAAATT</u> CAGTTAGACTCTG CTGATCTTCCCT <u>GCTAATTGAAGCACCGCGTTCTCGTCGGCATTGA</u> AGATCCC GTTATTGTTGCCATT <u>TTGTG</u>	6162
20	Waxy starch GBSS <i>Pisum sativum</i> Tyr18Term TAC-TAG	TTCAATT <u>AGCAAGGAAG</u>	6163
		CTTCCCTT <u>GCTAATTGAA</u>	6164
		TCTACACCGGAGAGAGCACC <u>ATGGCAACTGTAATAGCTGCACATT</u> TCGTTTCCAGGAG <u>CTGACACTTGAGCATCCATGCATTAGAGACTAA</u> GGCTAATAATT <u>GTCTCACACTGGACCTG</u>	6165
		CAGGGTC <u>CA GTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCAT</u> GGATGCT <u>CAAGTGTCAAGCTCTGGAAACGAAATGTGCAGCTATT</u> CAGTTGCCATGGT <u>GCTCTCCGGTGTAGA</u>	6166
25	Waxy starch GBSS <i>Manihot esculenta</i> Ser14Term TCA-TGA		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAGGAGCT <u>G</u> ACACTTGA	6167
	TCAAGTGT <u>C</u> AGCTCCTG	6168
5 Waxy starch GBSS <i>Manihot esculenta</i> Leu16Term TTG-TAG	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTGTT CCAGGAGCTCACACT <u>A</u> GAGCATCCATGCATTAGAGACTAAGGCTA ATAATTGTCACACTGGACCCCTGGACCCA TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTA ATGCATGGATGCT <u>T</u> AGTGTGAGCTCCTGGAAACGAAATGTGCAG CTATTACAGTTGCCATGGTGCCTCTCCGG CTCACACT <u>A</u> GAGCATCC GGATGCT <u>T</u> AGTGTGAG	6169 6170 6171 6172
10 Waxy starch GBSS <i>Manihot esculenta</i> Leu21Term TTA-TGA	TGGCAACTGTAATAGCTGCACATTGTTCCAGGAGCTCACACTT GAGCATCCATGCAT <u>G</u> AGAGACTAAGGCTAATAATTGTCACACT GGACCCCTGGACCCAAACTATCACTCCCAA TTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAGACAAATT TTAGCCTTAGTCT <u>C</u> ATGCATGGATGCTCAAGTGTGAGCTCCTGG AAACGAAATGTGCAGCTATTACAGTTGCCA CCATGCAT <u>G</u> AGAGACTA TAGTCT <u>C</u> ATGCATGG	6173 6174 6175 6176
15 Waxy starch GBSS <i>Manihot esculenta</i> Glu22Term GAG-TAG	GCAACTGTAATAGCTGCACATTGTTCCAGGAGCTCACACTTGA GCATCCATGCATT <u>A</u> GACTAAGGCTAATAATTGTCACACTGG ACCCCTGGACCCAAACTATCACTCCCAAATG CATTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAGACAAAT TATTAGCCTTAGTCT <u>A</u> TAATGCATGGATGCTCAAGTGTGAGCTCCT GGAAACGAAATGTGCAGCTATTACAGTTGC ATGCATT <u>A</u> GACTAAG CTTAGTCT <u>A</u> TAATGCAT	6177 6178 6179 6180
20 Waxy starch GBSS <i>Manihot esculenta</i> Lys24Term AAG-TAG	GTAATAGCTGCACATTGTTCCAGGAGCTCACACTTGAGCATCC ATGCATTAGAGACT <u>T</u> AGGCTAATAATTGTCACACTGGACCCCTG GACCCAAACTATCACTCCCAAATGGTTAA TTAAACCATTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAG ACAAATTATTAGCCT <u>A</u> GTCTCAATGCATGGATGCTCAAGTGTGA GCTCCTGGAAACGAAATGTGCAGCTATTAC TAGAGACT <u>T</u> AGGCTAAT ATTAGCCT <u>A</u> AGTCTCTA	6181 6182 6183 6184

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Phaseolus vulgaris</i> Ser12Term TCA-TGA	ACAACTCCTCCGTACCGGTATAAGCATGGCAACGGTATCGATGG CATCGTGCCTGGCGT <u>GAAAAGGCGCGTGGAGTACAGAGACAAAA</u> GTGAAATCTCGGGTCAGATGAGCCTGAACCG	6185
		CGGTCAGGCTCATCTGACCCGAAGATT <u>CACTTTGTCTCTGTAC</u> TCCACGCCCTTT <u>CACGCCACGCACGATGCCATCGATACCGTTG</u> CCATGCTTATACCGGTGACGGAGGAGTTGT	6186
		CGTGGCGT <u>GAAAAGGCG</u>	6187
		CGCCTTT <u>CACGCCACG</u>	6188
		CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCCTGGC GTCAAAAGGCGCGT <u>GAA</u> GTACAGAGACAAAAGTGAATCTCGGG TCAGATGAGCCTGAACCGCTCATGAATTGAAA	6189
10	Waxy starch GBSS <i>Phaseolus vulgaris</i> Trp16Term TGG-TGA	TTCAATT <u>CATGACGGTT</u> CAGGCTCATCTGACCCGAAGATT <u>CACT</u> TTTGTCTCTGTACT <u>TCACGCCCTTTGACGCCACGCACGATGCC</u> ATCGATA <u>ACCGTTGCCATGCTTATACCGGTG</u>	6190
		GGCGCGT <u>GAA</u> GTACAGA	6191
		TCTGTACT <u>TCACGCC</u>	6192
		ATAAGCATGGCAACGGTATCGATGGCATCGTGCCTGGCGTCAAA GGCGCGTGGAGTACAT <u>AGACAAAAGTGAATCTCGGGTCAGATG</u> AGCCTGAACCGCTCATGAATT <u>GAAATACGATG</u>	6193
		CATCGTATT <u>CAATT</u> CATGACGGTT <u>CAGGCTCATCTGACCCGAAGA</u> TTTCACTTT <u>GTCT</u> <u>ATGTACTCCACGCCCTTTGACGCCACGCAC</u> GATGCCATCGAT <u>ACCGTTGCCATGCTTAT</u>	6194
15	Waxy starch GBSS <i>Phaseolus vulgaris</i> Glu19Term GAG-TAG	GGAGTACAT <u>AGACAAAA</u>	6195
		TTTGTCT <u>ATGTACTCC</u>	6196
		ATGGCAACGGTATCGATGGCATCGTGCCTGGCGTCAAAAGGCGC GTGGAGTACAGAGACAT <u>AAGTGAATCTCGGGTCAGATGAGCCT</u> GAACCGTCATGAATT <u>GAAATACGATGGGTTGA</u>	6197
		TCAACCCATCGTATT <u>CAATT</u> CATGACGGTT <u>CAGGCTCATCTGACC</u> CGAAGATT <u>CACTT</u> <u>ATGTCTCTGTACTCCACGCCCTTTGACGCC</u> ACGCACGATGCCATCGAT <u>ACCGTTGCCAT</u>	6198
		CAGAGACAT <u>AAGTGA</u> AAA	6199
20	Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys21Term AAA-TAA	TTTCACTT <u>ATGTCTCTG</u>	6200
		ACGGTATCGATGGCATCGTGCCTGGCGTCAAAAGGCGCGTGGAG TACAGAGACAAAAGT <u>GTAA</u> TT <u>CTCGGGTCAGATGAGCCTGAACCG</u> TCATGAATT <u>GAAATACGATGGGTTGAGATCTC</u>	6201
		GAGATCTCAACCCATCGTATT <u>CAATT</u> CATGACGGTT <u>CAGGCTCAT</u> CTGACCCGAAGATT <u>ACACTTTGTCTGTACTCCACGCCCTTT</u> GACGCCACGCACGATGCCATCGAT <u>ACCGT</u>	6202
25	Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys23Term AAA-TAA		

SEQ ID NO.	Altering Oligos	Phenotype, Gene, Plant & Targeted Alteration
6203	CAAAAGTGTAAATCTTCG	
6204	CGAAGATT <u>A</u> CACTTTG	
6205	GCGCCTAGCTCGAAAAGGTCGTATTGAGAGGGCTGCACCAATGG GTTCCATTCTAATT <u>AG</u> TGTTCTTATCAAACAAACAGTGTGGTTCA CTGAAACTGTCGCCTCACATCCAATTCCAG	Waxy starch GBSS <i>Triticum aestivum</i>
6206	CTGGAATTGGATGTGAGGCGACAGTTCAAGTGAACCAACACTGTT GTTTGATAAGAACACTAATTAGGAATGGAACCCATTGGTGCAGCCT CTCAATGACGACCTTTGAGCTAGGCGC	Tyr7Term TAT-TAG
6207	CCTAATT <u>AG</u> TGTTCTTA	
6208	TAAGAAC <u>AC</u> TAATTAGG	
6209	CCTAGCTCGAAAAGGTCGTATTGAGAGGGCTGCACCAATGGGTC CATTCTAATTATT <u>G</u> ATCTTATCAAACAAACAGTGTGGTTCACTGA AACTGTGCCCTCACATCCAATTCCAGCAA	Waxy starch GBSS <i>Triticum aestivum</i>
6210	TTGCTGGAATTGGATGTGAGGCGACAGTTCAAGTGAACCAACACT GTTTGTTGATAAG <u>A</u> CAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTGAGCTAGG	Cys8Term TGT-TGA
6211	AATTATT <u>G</u> ATCTTATCA	
6212	TGATAAG <u>A</u> CAATAATT	
6213	TCGAAAAGGTCGTATTGAGAGGGCTGCACCAATGGGTCATTCC TAATTATTGTTCTT <u>AG</u> CAAACAAACAGTGTGGTTCACTGAAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT	Waxy starch GBSS <i>Triticum aestivum</i>
6214	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTCAAGTGAACC AACACTGTTGTTG <u>CTA</u> AGAACATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTGCA	Tyr10Term TAT-TAG
6215	TGTTCTT <u>AG</u> CAAACAAA	
6216	TTTGTGG <u>CTA</u> AGAACAA	
6217	CGAAAAGGTCGTATTGAGAGGGCTGCACCAATGGGTCATTCT AATTATTGTTCTT <u>AA</u> ACAAACAGTGTGGTTCACTGAAACTGTC GCCTCACATCCAATTCCAGCAATCTTGT	Waxy starch GBSS <i>Triticum aestivum</i>
6218	TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTCAAGTGAAC CAACACTGTTGTT <u>AA</u> TAAGAACATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTGCA	Gln11Term CAA-TAA
6219	GTTCTT <u>AA</u> ACAAAC	
6220	TTTGTGG <u>AA</u> TAAGAAC	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Triticum aestivum</i> Ser17Term TCA-TGA	AGGCTGCACCAATGGGTTCCATTCTAATTATTGTTCTTATCAAACA AACAGTGTGGTT <u>G</u> ACTGAAACTGTGCGCTCACATCCAATTCCAGC AATCTTGTAAACAATGAAGTTATGTTCCCT	6221
	AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAG GCGACAGTTTCAGT <u>C</u> AACCAACACTGTTGTTGATAAGAACATA ATTAGGAATGGAACCCATTGGTGCAGCCT	6222
	TGTTGGTT <u>G</u> ACTGAAAC	6223
	GTITCAGT <u>C</u> AACCAACA	6224
10 Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTT <u>C</u> TAGGGCGTGAGGCCCGGAGGCCGGCG GATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA	6225
	TAGCTCCGACGGTCTCATGCCGAGAGCCGCATCCGCCGGGCTC CGGGGCCTCACGCCCT <u>A</u> GAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6226
	CAGGTTT <u>C</u> AGGGCGTG	6227
	CACGCCCT <u>A</u> GAAACCTG	6228
	GGTTTCCAGGGCGTGAGGCCCGGAGGCCGGATGCGGCTC TCGGCATGAGGACCGT <u>C</u> TGAGCTAGCGCCGCCAACGCAAAGC CGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	6229
15 Waxy starch GBSS <i>Triticum aestivum</i> Gly46Term GGA-TGA	AGAGGCACCGCCGGTCCCGCGGTGCGCTTCCGGCTTGCCTT GGGGCGGCGCTAGCT <u>C</u> AGACGGTCTCATGCCGAGAGCCGCATC CGCCGGGCTCCGGGCTCACGCCCTGGAAACC	6230
	GGACCGT <u>C</u> TGAGCTAGC	6231
	GCTAGCT <u>C</u> AGACGGTCC	6232
	CGGAGCCCGGGGATGCGGCTCTCGGCATGAGGACCGTCGGAG CTAGCGCCGCCAACG <u>T</u> AAAGCCGGAAAGCGCACCGCGGGACC CGGCGGTGCCTCTCATGGTGGTGCACGCCACCG	6233
	CGGTGGCGCGCACCAACATGGAGAGGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTT <u>A</u> CGTTGGGCGCGTAGCTCCGACGG TCCTCATGCCGAGAGCCGCATCCGCCGGCTCCG	6234
20 Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CCCCAACG <u>T</u> AAAGCCGG	6235
	CCGGCTT <u>A</u> CGTTGGGG	6236
	GGGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCG CCCCAACGCAAAGCCGG <u>T</u> AAGCGCACCGCGGGACCCGGCGGTG CCTCTCCATGGTGGTGCACGCCACCGCAGCGCG	6237
	CGCCGCTGCCGGTGGCGCGCACCAACATGGAGAGGGACCCGCCG GGTCCC CGGGTGCCT <u>A</u> CCGGCTTGCCTGGGGCGCGTAG CTCCGACGGTCTCATGCCGAGAGCCGCATCCGC	6238

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAGCCGGTAAGCGCAC	6239
	GTGCGCTTACCGGCTT	6240
Waxy starch GBSS <i>Triticum aestivum</i>	CTCTCCATGGTGGTGCAGCGGCCACCGGCAGCGGGCGCATGAACCT CGTGTTCGTCGGCGCCTAGATGGCGCCCTGGAGCAAGACCGGGCG GCCTCGGCGACGTCTCGGGGGCCTCCCCCAG	6241
Glu85Term GAG-TAG	CTGGGGGGAGGCCCCCGAGGACGTCGCCGAGGCCGCCGGTCTT GCTCCAGGGCGCCATCTAGGCGCCGACGAACACGAGGTTATGC CGCCGCTGCCGGTGGCGCGACCACCATGGAGAG	6242
	TCGGCGCCTAGATGGCG	6243
	CGCCATCTAGGCGCCGA	6244
Waxy starch GBSS <i>Triticum aestivum</i>	GTCGTCTCTGCTGCAGGTAGCCACACCCCTGCAGCGCGATGGC GGCTCTGGTCACGTCGTAGCTGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGCAGGTTTC	6245
Gln8Term CAG-TAG	GAAAACCTGCACGCCGGAACCTGTCGGTATGCCGAGGACGGTG CCGGAGGTGGCGAGCTACGACGTGACCAGAGCCGCCATCGCGC GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC	6246
	TCACGTCGTAGCTCGCC	6247
	GGCGAGCTACGACGTGA	6248
Waxy starch GBSS <i>Triticum aestivum</i>	CAGCTGCCACCTCCGGCACCGTCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTTAGGGTGTGAGGCCCGGAGGCCGGCAG ATGCGCCGCTGGCATGAGGACTACCGGAGCGA	6249
Gln28Term CAG-TAG	TCGCTCCGGTAGTCCTCATGCCGAGCGCGCATCTGCCGGCTC CGGGGCCTCACACCCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6250
	CAGGTTTTAGGGTGTG	6251
	CACACCCCTAAAAACCTG	6252
Waxy starch GBSS <i>Triticum aestivum</i>	CCCCGGAGCCCGGCAGATGCCGCTGGCATGAGGACTACCG GAGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCCTCTCCATGGTGGTGCAGCG	6253
Lys52Term AAG-TAG	CGCGCACCACTGGAGAGGCACCGCCGGTCCCAGGGTGC TTCCGGCTTGTGCTACGGGGCGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGCGCATCTGCCGGCTCCGGGG	6254
	CCGCCCCGTAGCAACAA	6255
	TTGTTGCTACGGGGCGG	6256

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGAAG <u>T</u> AACAAAGCCGGAAAGCGCACCGCG GACCCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6257
	TGGCGCGCACCAACC <u>T</u> GGAGAGGCACCGCCGGTCCCGCG CGCTTCCGGCTTGT <u>T</u> ACTCGGGCGGCATCGCTCCGGTAG TCCTCATGCCGAGCGGCATCTGCCGGCTCCG	6258
	CCCCGAAG <u>T</u> AACAAAGC	6259
	GCTTGT <u>T</u> ACTCGGGG	6260
10 Waxy starch GBSS <i>Triticum aestivum</i> Gln54Term CAA-TAA	AGCCCAGGAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGAAG <u>C</u> AATAAAGCCGGAAAGCGCACCGCG CCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6261
	CCGTGGCGCGCACCAACC <u>T</u> GGAGAGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTT <u>T</u> ATTGCTCGGGCGGCATCGCTCCGG TAGTCCTCATGCCGAGCGGCATCTGCCGGCT	6262
	CGAAG <u>C</u> AATAAGCCGG	6263
	CCGGCTT <u>T</u> ATTGCTTCG	6264
	CAGCTGCCACCTCCGGCACCGCCTCGGCATCACCGACAGGTT CCGGCGTGAGGTT <u>T</u> AGGGCGTGAGGCCCGGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCGGCCGGTT CGGGGCCTCACGCC <u>T</u> AGAAACCTGCACGCCGGAACCTGTCGG GATGCCGAGGACGGTGCCTGGAGGTGGCGAGCTG CAGGTT <u>T</u> AGGGCGTG	6265 6266 6267 6268
15 Waxy starch GBSS <i>Triticum durum</i> Gln28Term CAG-TAG	CCCCGGAACCCGGCGATGCGGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCG <u>T</u> AGCAAAGCCGGAAAGCGCACCGCG AGCCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6269
	TGGCGCGCACCAACC <u>T</u> GGAGAGGCACCGCCGGTCCCGCG CGCTTCCGGCTT <u>T</u> ACGGGGCGCGCTCGCTCCGATAGTCC TCATGACGAGGGCCGCATCGGCCGGTTCCGGGG	6270
	CCGCCCC <u>T</u> AGCAAAGC	6271
	GCTTGT <u>T</u> ACGGGGCGG	6272
	CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCG <u>T</u> AAAGCCGGAAAGCGCACCGCG CGGCGGTGCCTCTCCATGGTGGTGCACGCCA CCGTGGCGCGCACCAACC <u>T</u> GGAGAGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTT <u>T</u> ACTCGGGCGCGCTCGCTCCGATAG TCCTCATGACGAGGGCCGCATCGGCCGGTTCCG	6273 6274

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Triticum durum</i> Lys56Term AAA-TAA	CCCCGAAG <u>TAAAGCCGG</u>	6275
	CCGGCTT <u>TACTCGGGGG</u>	6276
	GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC CCCGAAGCAAAGCCGG <u>TAAAGCGCACCGCGGGAGCCGGCGGTGC</u> CTCTCCATGGTGGTGCACGCCACGGCAGCGCG	6277
	CGCCGCTGCCGTGGCGCGCACACCATGGAGAGGGCACCGCCG GCTCCCGCGGTGCGCTT <u>ACCGGGCTTGCTTCGGGGCGCGCTCG</u> CTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	6278
	AAAGCCGG <u>TAAAGCGCAC</u>	6279
	GTGCGCTT <u>ACCGGGCTT</u>	6280
	TATCGGAGCGAGCGCCGCCCGAAGCAAAGCCGGAAAGCGCAC GCGGGAGCCGGCGGTG <u>ACTCTCCATGGTGGTGCACGCCACGGG</u> CAGCGGCCGGCATGAACCTCGTGTTCGTCGGCGCC	6281
	GGCGCCGACGAACACGAGGTTATGCCGCCGTGCCGTGGCG CGCACCAACCATGGAGAGTCACCGCCGGCTCCCGCGTGCCTT CCGGCTTGCTTCGGGGCGCTCGCTCCGATA	6282
	CGGCGGTG <u>ACTCTCCAT</u>	6283
	ATGGAGAG <u>TACCCGCCG</u>	6284
10 Waxy starch GBSS <i>Triticum durum</i> Cys64Term TGC-TGA	CAGCTCGCCACCTCCGGCACCGTCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTT <u>TAGGGTGTGAGGGCCCGAGCCGGCAG</u> ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6285
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCATCTGCCGGGCTC CGGGGCCTCACACCC <u>TAAAAACCTGCACGCCGGAACCTGTCGGT</u> GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6286
	CAGGTTT <u>TAGGGTGTG</u>	6287
	CACACCC <u>TAAAAACCTG</u>	6288
	CCCCGGAGCCGGCAGATGCGCCGCTCGGCATGAGGACTACCG GAGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGCACG	6289
15 Waxy starch GBSS <i>Triticum turgidum</i> Lys52Term AAG-TAG	CGCGCACCACCATGGAGAGGGCACCGCCGGTCCCACGGTGCACG TTTCCGGCTTGCT <u>ACGGGGCGCGCTCGCTCCGGTAGTCC</u> TCATGCCGAGCGGCATCTGCCGGCTCCGGG	6290
	CCGCCCC <u>GTAGCAACAA</u>	6291
	TTGTTGCT <u>ACGGGGCGG</u>	6292

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Triticum turgidum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGAAG <u>T</u> AACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6293
	TGGCGCGCACCAACC <u>T</u> GGAGAGGGCACCGCCGGTCCCACGG CGCTTCCGGCTT <u>T</u> ACTCGGGCGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGCGCATCTGCCGGCTCCG	6294
	CCCCGAAG <u>T</u> AACAAAGC	6295
	GCTTTGTT <u>T</u> ACTCGGGG	6296
10 Waxy starch GBSS <i>Triticum turgidum</i> Gln54Term CAA-TAA	AGCCCAGGAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGAAG <u>C</u> AATAAAGCCGGAAAGCGCACCGCGGGAC CCGGCGGTGCCTCTCCATGGTGGTGCACGCCACCG	6297
	CCGTGGCGCGCACCAACC <u>T</u> GGAGAGGGCACCGCCGGTCCCACGG GTGCGCTTCCGGCTT <u>T</u> ATTGCTTCGGGGCGCGCTCGCTCCGG TAGTCCTCATGCCGAGCGCGCATCTGCCGGCT	6298
	CGAAG <u>C</u> AATAAGCCGG	6299
	CCGGCTT <u>T</u> ATTGCTTCG	6300
	Waxy starch GBSS <i>Triticum turgidum</i> Lys57Term AAA-TAA	6301
15 Waxy starch GBSS <i>Triticum turgidum</i> Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCC CGAAC <u>A</u> AAAGCCGG <u>T</u> AAGCGCACCGCAGGGACCCGGCGGT CCTCTCCATGGTGGTGCACGCCACGGCAGCGCCG	6302
	CGGCGCTGCCGTGGCGCGCACCAACC <u>T</u> GGAGAGGGCACCGCCG GGTCCCACGGTGCCT <u>T</u> ACCGGCTT <u>T</u> GTGCTTCGGGGCGCGC TCGCTCCGGTAGTCCTCATGCCGAGCGCGCATC	6303
	AAAGCCGG <u>T</u> AAGCGCAC	6304
	GTGCGCTT <u>T</u> ACCGGCTT	6305
	Waxy starch GBSS <i>Aegilops speltoides</i> Gln28Term CAG-TAG	6306
20 Waxy starch GBSS <i>Aegilops speltoides</i> Gln28Term CAG-TAG	CAGCTGCCACCTCCGCCACCGTCTCGGCATCACCGACAGGTT CCGCCATGCA <u>G</u> GGTT <u>T</u> AGGGCGTGAGGCCCGGAGCCGGCAG ATGCGCCGCTCGGCATGAGGACTGTGGAGCGA	6307
	TCGCTCCGACAGTCCTCATGCCGAGCGCGCATCTGCCGGGCTC CGGGGCCTCACGCC <u>T</u> AGAAACCTGCATGGCGAACCTGTGGT GATGCCGAGGACGGTGGCGAGGTGGCGAGCTG	6308
	CAGGTT <u>T</u> CA <u>G</u> GGCGTG	6309
	CACGCC <u>T</u> AGAAACCTG	6310
25 Waxy starch GBSS <i>Aegilops speltoides</i> Gly46Term GGA-TGA	GGTTCCAGGGCGTGAGGCCCGGAGCCGGCAGATGCGCCGC TCGGCATGAGGACTGT <u>T</u> AGCGAGCGCCGCCCGAACAA AGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCC	6311
	GGCACCGCCGGGTCCCGCGGTGCCTTCCGGCTTGTGCTTC GGGGCGCGCTCGCT <u>A</u> GACAGTCCTCATGCCGAGCGCGCAT	6312
	CTGCCGGCTCCGGGCTCACGCC <u>T</u> GGAAACC	6313

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGACTGTCTGAGCGAGC	6311
	GCTCGCTC <u>A</u> GACAGTCC	6312
5 Waxy starch GBSS <i>Aegilops speltoides</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTGCG GAGCGAGCGCCGCCCCG <u>T</u> AGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCGATGGTGGTGCACG CGCGCACCAACCATCGAGAGGCACCAGCCGGTCCCACGGTGCACG TTTCCGGCTTTGTT <u>A</u> CGGGGGCGCGCTCGCTCCGACAGTCC TCATGCCGAGCGGCATCTGCCGGCTCCGGG CCGCCCCG <u>T</u> AGCAACAA	6313 6314 6315 6316
10 Waxy starch GBSS <i>Aegilops speltoides</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTGGAG CGAGCGCCGCCCCG <u>A</u> AGTAACAAAGCCGGAAAGCGCACCACGG GACCCGGCGGTGCCTCTCGATGGTGGTGCACG TGGCGCGCACCAACCATCGAGAGGCACCAGCCGGTCCCACGGTGCACG CGCTTTCCGGCTTTGTT <u>A</u> CTTCCGGGGCGCTCGCTCCGACAG TCCTCATGCCGAGCGGCATCTGCCGGCTCCG CCCCGAAG <u>T</u> AAACAAAGC GCTTTGTT <u>A</u> CTTCCGGG	6317 6318 6319 6320
15 Waxy starch GBSS <i>Aegilops speltoides</i> Gln54Term CAA-TAA	AGCCCGGGCAGATGCGCCGCTCGGCATGAGGACTGTGGAGCGA GCGCCGCCCCG <u>A</u> AGCAAAAGCCGGAAAGCGCACCACGG CCGGCGGTGCCTCTCGATGGTGGTGCACG CGGTGGCGCGCACCAACCATCGAGAGGCACCAGCCGGTCCCACGG GTGCGCTTCCGGCTTT <u>A</u> TTGCTTCCGGGGCGCGCTCGCTCCGA CAGTCCTCATGCCGAGCGGCATCTGCCGGCT CGAAGCAAAAGCCGG CCGGCTT <u>A</u> TTGCTTCG	6321 6322 6323 6324
20 Waxy starch GBSS <i>Oryza glaberrima</i> Gln8Term CAG-TAG	AGTCAGAGATCTTCCACAGCAACAGCTAGACAACCACATGTG GCTCTCACCAACGTC <u>T</u> AGCTGCCACCTCGGCCACCGGCTTCGG CATCGCTGACAGGTGGCGCCGTGCGCTGC GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCT <u>A</u> GGACGTGGTGAAGAGCCGACATGGT GTTGTCTAGCTGTTGCTGGAAGATCTCTGCACT CCACGTCC <u>T</u> AGCTCGCC GGCGAGCT <u>A</u> GGACGTGG	6325 6326 6327 6328

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Oryza glaberrima</i> Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAAACCACCATGTCGGCTCTCACCACGT CCCAGCTGCCACCT <u>AGGCCACCGGCTCGGCATCGCTGACAGG</u> TCGGCGCCGTCGCTGCTGCCACGGGTT	6329
	AACCCGTGGCGGAGCAGCGACGACGGCGCCACCTGTCAGCGAT GCCGAAGCCGGTGGCT <u>AGGTGGCGAGCTGGGACGTGGTGAGA</u> GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	6330
	CGCCACCT <u>AGGCCACCG</u>	6331
	CGGTGGCT <u>AGGTGGCG</u>	6332
	CGGCTCTACCACGTCCAGCTGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGT <u>AGGCACCGTCGCTGCTGCTCCGCCACGG</u> GTTCAGGGCCTCAAGCCCCGAGCCCCGCC	6333
Waxy starch GBSS <i>Oryza glaberrima</i> Ser22Term TCG-TAG	CCGGCGGGGCTGCGGGCTTGAGGCCCTGGAACCCGTGGCGGA GCAGCGACGACGGCGCCT <u>ACCTGTCA</u> CGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6334
	TGACAGGT <u>AGGCACCGT</u>	6335
	ACGGCGCCT <u>ACCTGTCA</u>	6336
	CCACGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTGGCGCCGT <u>AGTCGCTGCTCCGCCACGGGTTCCAGG</u> GCCTCAAGCCCCGAGCCCCGCCGGCGACGC	6337
	GCGTCGCCGCCGGCGGGCTGCGGGGCTTGAGGCCCTGGAACC CGTGGCGGAGCAGCGACT <u>ACGGCGCCGACCTGTCA</u> CGCGATGCC GAAGCCGGTGGCCAGGGTGGCGAGCTGGGACGTGG	6338
Waxy starch GBSS <i>Oryza glaberrima</i> Ser25Term TCG-TAG	GGCGCCGT <u>AGTCGCTGC</u>	6339
	GCAGCGACT <u>ACGGCGCC</u>	6340
	CGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTGGCGCCGT <u>AGTCGCTCCGCCACGGGTTCCAGGGCCT</u> CAAGCCCCGAGCCCCGCCGGCGACGC	6341
	GTCGCGTCGCCGCCGGCGGGCTGCGGGGCTTGAGGCCCTGGA ACCGTGGCGAGCAGCGACT <u>ACGACGGCGCCGACCTGTCA</u> CGCGATG CCGAAGCCGGTGGCCAGGGTGGCGAGCTGGGACG	6342
	GCCGTCGT <u>AGTCGCTCC</u>	6343
Waxy starch GBSS <i>Oryza sativa</i> Gln8Term CAG-TAG	GGAGCAGCT <u>ACGACGGC</u>	6344
	TCCACAGCAAGAGCTAACAGCCGACCGTGTGCACCAACCATGTCG GCTCTACCACGTCT <u>AGCTCGCCACCTCGGCCACCGGCTTCGG</u> CATGCCGACAGGTGGCGCCGT <u>CGCTG</u>	6345
	GCAGCGACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCT <u>AGGACGTGGTGAGAGCCGACATGGT</u> GTGCACACGGTCGGCTGTTAGCTTGTGCTGTGGA	6346

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CCACGTCC <u>T</u> AGCTCGCC	6347
	GGCGAGCT <u>A</u> GGACGTGG	6348
Waxy starch GBSS <i>Oryza sativa</i> Ser12Term TCG-TAG	CTAAACAGCCGACC <u>G</u> TGTGCACCACCATGT <u>C</u> GGCTCTCAC <u>C</u> CGAC CCCAGCTCGCC <u>C</u> AC <u>C</u> TA <u>G</u> GC <u>C</u> ACCG <u>G</u> GCTTC <u>G</u> GCATCGCC <u>G</u> ACAGG TCGGCGCC <u>G</u> TC <u>G</u> CTGCTG <u>C</u> CTCGCC <u>C</u> ACGGGTT AACCCGTGG <u>C</u> GAAGCAG <u>C</u> GCAC <u>G</u> GG <u>C</u> CC <u>G</u> AC <u>C</u> CTGT <u>C</u> GG <u>C</u> GAT GCC <u>G</u> A <u>G</u> CC <u>G</u> GTGG <u>C</u> CT <u>A</u> GG <u>T</u> GG <u>C</u> GAG <u>T</u> GG <u>C</u> GAC <u>T</u> GG <u>G</u> AC <u>T</u> GG <u>T</u> GAGA GCC <u>G</u> AC <u>A</u> CTGG <u>T</u> GG <u>G</u> CAC <u>A</u> GG <u>T</u> GG <u>C</u> GT <u>T</u> TTAG CGCC <u>A</u> CC <u>T</u> AG <u>G</u> CC <u>A</u> CC <u>G</u>	6349 6350 6351 6352
Waxy starch GBSS <i>Oryza sativa</i> Ser22Term TCG-TAG	CGGCTCTACCAC <u>G</u> CCC <u>A</u> G <u>C</u> CT <u>C</u> GG <u>C</u> AC <u>C</u> CG <u>G</u> CTTC GG <u>C</u> AT <u>C</u> GG <u>C</u> GC <u>A</u> CG <u>G</u> T <u>A</u> GG <u>G</u> CC <u>G</u> TC <u>G</u> CT <u>G</u> CT <u>C</u> GG <u>C</u> AC <u>G</u> G GTT <u>C</u> AG <u>GG</u> GC <u>T</u> CA <u>G</u> CCC <u>G</u> T <u>A</u> GG <u>CC</u> CG <u>C</u> AG <u>CC</u> CG CCGGCTGG <u>C</u> T <u>A</u> GG <u>GG</u> CT <u>T</u> G <u>A</u> GG <u>CC</u> CT <u>G</u> GA <u>AC</u> CC <u>G</u> T <u>GG</u> CG <u>A</u> GC <u>A</u> GC <u>G</u> AC <u>G</u> AC <u>GG</u> GC <u>C</u> <u>T</u> AC <u>C</u> CT <u>G</u> CG <u>C</u> G <u>A</u> T <u>G</u> CC <u>G</u> A <u>AG</u> CC <u>GG</u> GCC <u>G</u> AG <u>G</u> T <u>GG</u> CG <u>A</u> G <u>C</u> T <u>GG</u> AC <u>G</u> T <u>GG</u> T <u>GG</u> GAG <u>G</u> CC <u>G</u> CG <u>A</u> C <u>AG</u> GT <u>A</u> GG <u>G</u> CC <u>G</u> T ACGGCG <u>C</u> <u>T</u> AC <u>C</u> CT <u>G</u> TC <u>G</u>	6353 6354 6355 6356
Waxy starch GBSS <i>Oryza sativa</i> Ser25Term TCG-TAG	CCACGTCCC <u>A</u> G <u>C</u> CT <u>C</u> GG <u>C</u> AC <u>C</u> CT <u>C</u> GG <u>C</u> AC <u>C</u> GG <u>G</u> CTTC <u>G</u> GC <u>A</u> TC <u>G</u> CC GAC <u>AG</u> GT <u>GG</u> CG <u>C</u> CG <u>T</u> <u>A</u> GT <u>C</u> GT <u>G</u> CT <u>T</u> CG <u>C</u> AC <u>GG</u> TT <u>CC</u> AG <u>GG</u> CCT <u>A</u> AG <u>GG</u> CC <u>C</u> CG <u>T</u> AG <u>CC</u> CA <u>G</u> CC <u>GG</u> CG <u>GG</u> GA <u>C</u> GC CGT <u>CC</u> CC <u>G</u> CC <u>GG</u> CT <u>GG</u> CT <u>A</u> CG <u>GG</u> CT <u>T</u> G <u>A</u> GG <u>CC</u> CT <u>GG</u> AC <u>C</u> CG <u>T</u> GG <u>C</u> GA <u>AG</u> C <u>A</u> GC <u>G</u> ACT <u>A</u> CG <u>GC</u> CC <u>G</u> AC <u>C</u> CT <u>G</u> CG <u>C</u> G <u>A</u> T <u>G</u> CC GA <u>AG</u> CC <u>GG</u> T <u>GG</u> CC <u>G</u> AG <u>G</u> T <u>GG</u> CG <u>A</u> G <u>C</u> T <u>GG</u> AC <u>G</u> T <u>GG</u> GG <u>G</u> CC <u>C</u> GT <u>A</u> GT <u>C</u> GT <u>G</u> C GC <u>A</u> GC <u>G</u> ACT <u>A</u> CG <u>GG</u> GC <u>C</u>	6357 6358 6359 6360
Waxy starch GBSS <i>Oryza sativa</i> Ser26Term TCG-TAG	CGT <u>CC</u> CC <u>A</u> G <u>C</u> CT <u>C</u> GG <u>C</u> AC <u>C</u> CT <u>C</u> GG <u>C</u> AC <u>C</u> GG <u>G</u> CTTC <u>G</u> GC <u>A</u> TC <u>G</u> CC <u>G</u> AC AG <u>GT</u> CG <u>GG</u> CG <u>C</u> CG <u>T</u> <u>A</u> GT <u>C</u> GT <u>G</u> CT <u>T</u> CG <u>C</u> AC <u>GG</u> TT <u>CC</u> AG <u>GG</u> C <u>T</u> CA <u>AG</u> CC <u>CC</u> CG <u>T</u> AG <u>CC</u> CA <u>G</u> CC <u>GG</u> CG <u>GG</u> GA <u>C</u> GC <u>A</u> TC GAT <u>GC</u> GT <u>CC</u> CC <u>G</u> CC <u>GG</u> CT <u>GG</u> CT <u>A</u> CG <u>GG</u> CT <u>T</u> G <u>A</u> GG <u>CC</u> CT <u>GG</u> AA CC <u>CG</u> GT <u>GG</u> CG <u>A</u> AG <u>C</u> AG <u>C</u> T <u>A</u> CG <u>AC</u> GG <u>C</u> CC <u>G</u> AC <u>C</u> CT <u>G</u> CG <u>C</u> G <u>A</u> T <u>G</u> CC CG <u>A</u> AG <u>CC</u> GG <u>T</u> GG <u>CC</u> GA <u>GG</u> T <u>GG</u> CG <u>A</u> G <u>C</u> T <u>GG</u> AC <u>G</u>	6361 6362 6363 6364

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Hordeum vulgare</i> Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCCTGTGCGCGGCCATGGC GGCTCTGCCACGTCC <u>T</u> AGCTGCCACCTCCGGCACCGTCCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTC	6365
		GAAAACCTGGACGCCGGAATCTGTCGGTACGCCGAGGACGGTG CCGGAGGTGGCGAGCT <u>A</u> GGACGTGCCAGAGCCGCCATGGCGC	6366
		CGCGCACAGGTGTGGCTACCTGCAGTGAGAGAC	
		CCACGTCC <u>T</u> AGCTCGCC	6367
		GGCGAGCT <u>A</u> GGACGTGG	6368
10	Waxy starch GBSS <i>Hordeum vulgare</i> Arg21Term AGA-TGA	ATGGCGGCTCTGGCCACGTCCCAGCTGCCACCTCCGGCACCGT CCTCGGCGTCACCGAC <u>T</u> GATTCCGGCGTCCAGGTTTCAGGGCCT CAGGCCCCGGAACCCGGCGGATGCCGGCCTTG	6369
		CAAGCGCCGCATCCGCCGGTTCCGGGGCTGAGGCCCTGAAAA CCTGGACGCCGGAAT <u>C</u> AGTCGGTACGCCGAGGACGGTGCCGG	6370
		AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	
		TCACCGAC <u>T</u> GATTCCGG	6371
		CCGGAAT <u>C</u> AGTCGGTGA	6372
15	Waxy starch GBSS <i>Hordeum vulgare</i> Gln28Term CAG-TAG	CAGCTGCCACCTCCGGCACCGTCCTCGCGTCACCGACAGATT CCGGCGTCCAGGTTT <u>T</u> AGGGCCTCAGGCCCCGGAACCCGGCGG ATGCGGCCCTGGTATGAGGACTATCGGAGCAA	6373
		TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGTTCC GGGGCCTGAGGCC <u>T</u> AAAACCTGGACGCCGAATCTGTCGGTG	6374
		ACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	
		CAGGTTT <u>T</u> AGGGCCTC	6375
		GAGGCC <u>T</u> AAAACCTG	6376
20	Waxy starch GBSS <i>Hordeum vulgare</i> Gly46Term GGA-TGA	GGTTTCAGGGCCTCAGGCCCGGAACCCGGCGGATGCCGGCCT TGGTATGAGGACTAT <u>C</u> TGAGCAAGCGCCGCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCT	6377
		AGAGGCACCGCCGGCTCCCGCGGTGCGCTTCCGGCTTGCTC GGGGCGGCCTGCT <u>C</u> AGATAGTCCTCATACCAAGCGCCGCATC	6378
		CGCCGGGTTCCGGGGCTGAGGCCCTGAAAACC	
		GGACTAT <u>C</u> TGAGCAAGC	6379
		GCTTGCT <u>C</u> AGATAGTCC	6380
25	Waxy starch GBSS <i>Hordeum vulgare</i> Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCCGCCCTGGTATGAGGACTATCGG AGCAAGCGCCGCCCG <u>T</u> AGCAAAGCCGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGAAGCGCCA	6381
		TGGCGCTCACCACCGAGAGGCACCGCCGGCTCCGCCGGTG CGCTTCCGGCTTGCT <u>A</u> CGGGCGGCCGCTTGCTCCGATAGTCC	6382
		TCATACCAAGCGCCGCATCCGCCGGTTCCGGGG	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CCGCCCCGTAGCAAAGC	6383
	GCTTGCT <u>A</u> CGGGGCGG	6384
5 Waxy starch GBSS <i>Zea mays</i> Gln8Term CAG-TAG	ACGTCTTTCTCTCTCCTACGCAGTGGATTAAATGGCATGGCGG CTCTGGCCACGT <u>C</u> GTAGCTCGTCGCAACGCGCGCCGGCTGGC GTCCCAGCGCGTCCACGTTCCGCCGCGCG	6385
	CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCAGGCCGG GCGCGTTGCACGAG <u>C</u> ACGACGTGGCCAGAGCCGCCATGCCGA TTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT	6386
	CCACGTCGTAGCTCGTC	6387
	GACGAG <u>C</u> ACGACGTGG	6388
	GTCGCAACGCGGCCGGCTGGCGTCCCAGCGCGTCCACGT TCCGCCGCGGCCGCG <u>C</u> GTAGGGCCTGAGGGGGGCCGGCGTC GGCGCGCGGACACGCTCAGCATGCGGACCGAGCG	6389
10 Waxy starch GBSS <i>Zea mays</i> Gln30Term CAG-TAG	CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGACGCCCG GGCCCCCCTCAGGCC <u>C</u> ACGCGGCCGCCGCCGGAACGTGGAC GCGTCCGGGACGCCAGGCCGGCGCGTTCGAC	6390
	GCGCCGCG <u>C</u> TAGGGCCTG	6391
	CAGGCC <u>C</u> ACGCGGCC	6392
	TCCCGGACGCGTCCACGTTCCGCCGCCGCCGCAGGGCCT GAGGGGGGCCGGCG <u>C</u> TAAGCGGGCGGACACGCTCAGCATG CGGACCAAGCGGCCGCCGCCGCCAGGCACCAAGCA	6393
	TGCTGGTGCCTGGCGCCGCGCGCGCTGGTCCGCATGCTGA GCGTGTCCGCCGCC <u>C</u> ACGCCGGGCCCCCTCAGGCCCTG CGCGGCCGCCGCCGGAACGTGGACGCGTCCGGGA	6394
15 Waxy starch GBSS <i>Zea mays</i> Ser38Term TCG-TAG	CCGGGGCG <u>C</u> AGGCCGG	6395
	CCGCCGC <u>C</u> ACGCCGG	6396
	GCGTCGGCGGCCGGACACGCTCAGCATGCGGACCGAGCGCGC GCGCGGCC <u>C</u> AGGC <u>A</u> CGCAGCAGCGGCCGCCGGCA GGTCCCCGTCGCTCGTGTGCGCCAGCGCCGGCA	6397
	TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCC GCGGCGGCCCTGCTG <u>C</u> AGTGCCTGGCGCCGCCGCGCGCTG GTCCGCATGCTGAGCGTGTCCGCCGCCGACGC	6398
	CCAGGC <u>A</u> CTAGCAGCAG	6399
20 Waxy starch GBSS <i>Zea mays</i> Ser57Term CAG-TAG	CTGCTGCT <u>A</u> GTGCCTGG	6400

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS Zea mays Gln58Term CAG-TAG	TCGGCGGCGGGACACGCTCAGCATGCGGACAGCGCGCG CGCGCCCAGGCACCAGTAGCAGGCGCGCCGGGGCAGGTT CCCGTCGCTCGTCGTGCGGCCAGCGCCGGCATGA	6401
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGAACCTGCC CCGCAGCGCGCTGCTACTGGTGCCCTGGCGCCGCGCGCG TGGTCCGATGCTGAGCGTGTCCGCCGCCGA	6402
	GGCACCAGTAGCAGGCG	6403
	CGCCTGCTACTGGTGCC	6404

## Example 11

Altering fatty acid content of plants

Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearoyl- and oleoyl-ACP.

A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearoyl-acyl carrier protein (stearoyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

Table 22  
Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser8Term TCG-TAG	TTGGTGGCAGTGTCTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGT <del>A</del> GTCAATTCTTCCTGTACCATCTTCACTT GATCCTAATGGAAAAGGCAATAAGATTGG	6405
	CCAATCTTATTGCCTTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGACT <del>A</del> CGTAGCAGAGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAA	6406

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTACGT <u>A</u> GTCAATTCT	6407
	AGAATGACT <u>A</u> CGTAGCA	6408
5 Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser9Term TCA-TGA	GGTGGCAGTGTCTTGAACGCTTCATCTCCTCGTCATGGTGGCCA CCTCTGCTACGTCGT <u>G</u> ATTCTTCCTGTACCATCTTCTTCACTTGAT CCTAATGGAAAAGGCAATAAGATTGGGTC	6409
	GACCCAATCTTATTGCCCTTCCATTAGGATCAAGTGAAGAAGATG GTACAGGAAAGAAC <u>T</u> ACGACGTAGCAGAGGTGGCCACCATGACGA GGAGATGAAGCGTCAAAGACACTGCCACC	6410
	TACGTCGT <u>G</u> ATTCTTC	6411
	GAAAGAAC <u>T</u> ACGACGTA	6412
	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCAATTCTTC TGTACCATCTTCTT <u>G</u> ACTTGATCCTAATGGAAAAGGCAATAAGATT GGGTCTACGAATCTTGCTGGACTCAATT	6413
10 Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser17Term TCA-TGA	GAATTGAGTCCAGCAAGATT <u>C</u> GTAGACCCAATCTTATTGCCCTTTC CATTAGGATCAAGT <u>C</u> AAGAACATGGTACAGGAAAGAAC <u>T</u> ACGACG TAGCAGAGGTGGCCACCATGACGAGGGAGAT	6414
	ATCTTCTT <u>G</u> ACTTGATC	6415
	GATCAAGT <u>C</u> AAGAAC <u>T</u>	6416
	GTGGCCACCTCTGCTACGTCGTCAATTCTTCCTGTACCATCTTCTT CACTTGATCCTAATT <u>T</u> AAAAGGCAATAAGATTGGGTCTACGAATCT TGCTGGACTCAATTCTGCACCTAACTCTG	6417
	CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATT <u>C</u> GTAGACCCA TCTTATTGCCCTTTC <u>A</u> ATTAGGATCAAGTGAAGAACATGGTACAGG AAAGAAC <u>T</u> ACGACGTCAGCAGAGGTGGCCAC	6418
15 Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Gly22Term GGA-TGA	ATCCTAATT <u>T</u> AAAAGGC	6419
	GCCTTTC <u>A</u> ATTAGGAT	6420
	GCTTGAATTGTGATCTGATTGGTTAATTGTGGCCACAA <u>T</u> GGTTGC TACTGCCGCCACGT <u>G</u> ATCATTCTTCGTTGACTCCCTCTGGG GATGCCAAATCGGGCAATCCC <u>G</u> AAAAGG	6421
	CCTTTCCGGGATTGCCGATTGGCATCCCCAGAACGGGGAA <u>G</u> TC AACGGAAAGAAC <u>T</u> GT <u>C</u> ACGTGGCGGCAGTAGCAACCATTGTGGCC ACAATTAA <u>C</u> CAATCAGATCACAAATTCA <u>A</u> GC	6422
	CGCCACGT <u>G</u> ATCATTCT	6423
20 Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser8Term TCA-TGA	AGAATGAT <u>C</u> ACGTGGCG	6424

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser9Term TCA-TGA	TGAATTGTGATCTGATTGGTAATTGTGGCCACAATGGTTGCTAC TGCCGCCACGT <u>CATGATTCTTCCGTTGACTTCCCCTCTGGGGAT</u> GCCAAATCGGGCAATCCCAGAAAAGGGTC	6425
		GACCCTTTCCGGATTGCCCGATTGGCATCCCCAGAAGGGGAA GTCAACGAAAGAAT <u>CATGACGTGGCGGCAGTAGCAACCATTGTG</u> GCCACAATTAACCAATCAGATCACAAATTCA	6426
		CACGT <u>CATGATTCTTC</u>	6427
		GAAAGAAT <u>CATGACGTG</u>	6428
		CTGATTGGTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT CATCATTCTTCCG <u>TAGACTTCCCCTCTGGGGATGCCAAATCGG</u> GCAATCCCAGAAAAGGGTCGGTGAGTTTGG	6429
10	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Leu13Term TTG-TAG	CCAAAAC <u>TCACCGACCCTTCCGGATTGCCGATTGGCATCC</u> CCAGAAGGGGAAGT <u>CACGGAAAGAATGATGACGTGGCGGCAGT</u> AGCAACCATTGTGCCACAATTAACCAATCAG	6430
		CTTCCG <u>TAGACTTCCC</u>	6431
		GGGAAGT <u>CTACGGAAAG</u>	6432
		ATGGTTGCTACTGCCGCCACGT <u>CATCATTCTTCCGTTGACTTCCC</u> CTTCTGGG <u>GATGCC</u> <u>TAATCGGGCAATCCCAGAAAAGGGTCGG</u> AGTTTG <u>GGTCATGAAGTCGAAATCCGCGG</u>	6433
		CCGCGGATT <u>CGACTTCATTGACCCAAACTCACCGACCCTTCC</u> GGGATTGCCGATT <u>AGGCATCCCCAGAAGGGGAAGTCAACGGAA</u> AGAATGATGACGTGGCGGCAGTAGCAACCAT	6434
15	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Lys21Term AAA-TAA	GGGAT <u>GCCTAATCGGGC</u>	6435
		GCCCGATT <u>AGGCATCCC</u>	6436
		GGGATT <u>CGACGAAATTGAAGTTGTTTAAAAACCATGGTTGC</u> TACTGCTGTGACAT <u>AGGC</u> <u>GTTTCCCAGTC</u> <u>ACTTCTCACCTGAC</u> TCCTCTGACT <u>CGAAAACAAGAAGCTCGG</u>	6437
		CCGAGCTT <u>CTGTTTCGAGTCAGAGGAGTCAGGTGAAGAAGTG</u> ACTGGGAAA <u>ACGCC</u> <u>TATGTCACAGCAGTAGCAACCATGGTTTTA</u> AAAACA <u>ACTCAATTCTGTGCTGAAATCCC</u>	6438
		TGTGACAT <u>AGGC</u> <u>GTTT</u>	6439
20	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser8Term TCG-TAG	AAAACG <u>CC</u> <u>TATGTCACA</u>	6440
		TGTTTTAAAAACCATGGTTGCTACTGCTGTGACAT <u>CGGC</u> <u>TTTT</u> CCCAGTC <u>ACTTCTGACCTGACTCCTCTGACTCGAAAACAAGAAG</u> CTCGGAAG <u>CATCAAGTCGAAGCCATCGGT</u>	6441
		ACCGATGGCT <u>TCGACTTGATGCTTCCGAGCTTCTGTTTCGAGT</u> CAGAGGAGTC <u>AGGTCAAGAAGTGACTGGAAAACGCCATGTCA</u> CAGCAGTAG <u>CAACCATGGTTTAAAAACA</u>	6442
25	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser16Term TCA-TGA		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CACTTCTT <u>GACCTGACT</u>	6443
	AGTCAGGT <u>CAAGAAAGTG</u>	6444
Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser22Term TCG-TAG	TTGCTACTGCTGTGACATCGCGTTTCCCAGTCACCTCTCACCG TGACTCCTCTGACT <u>AGAAAAACAAGAAGCTCGGAAGCATCAAGTC</u> GAAGCCATCGGTTTCTTCTGGAAGTTGCA	6445
	TGCAAACCTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCGA GCTTCTTGT <u>TTCTAGTCAGAGGAGTCAGGTGAAGAAGTGA</u> CTGG GAAAAACGCCGATGTCACAGCAGTAGCAA	6446
	CTCTGACT <u>AGAAAAACA</u>	6447
	TG <u>TTTTCTAGTCAGAG</u>	6448
Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Lys23Term AAA-TAA	GCTACTGCTGTGACATCGCGTTTCCCAGTCACCTCTCACCTG ACTCCTCTGACT <u>CGTAAAACAAGAAGCTCGGAAGCATCAAGTCGA</u> AGCCATCGGTTTCTTCTGGAAGTTGCAAG	6449
	CTTGCAAACCTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCC GAGCTTCTTGT <u>TTACGAGTCAGAGGAGTCAGGTGAAGAAGTGA</u> C TGGGAAAAACGCCGATGTCACAGCAGTAGC	6450
	CTGACT <u>CGTAAAACAAG</u>	6451
	CTTGT <u>TTTACGAGTCAG</u>	6452
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Ser14Term TCG-TAG	CTCCCGCTCGTGAAGACAA <u>TGGTGGCTACCGCTGCAAGCTCG</u> CATTCTTCCCCGTG <u>TAGTCCCCGGTCACCTCCTCTAGACCAGGAA</u> AGCCCGGAA <u>ATGGGT</u> CATCGAGCTTCAGCCC	6453
	GGGCTGAAGCTCGATGACCC <u>ATTCCGGGCTTCCCTGGTCTAGAG</u> GAGGTGACC <u>GGGGACTACACGGGGAAAGAATGCAGAGCTTG</u> CAGC GGTAGCCACCATTGTCTTCAACGAGC <u>GGGAG</u>	6454
	CCCCGTG <u>TAGTCCCCGG</u>	6455
	CCGGGG <u>ACTACACGGGG</u>	6456
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Arg21Term AGA-TGA	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTCCCCGTGCGTCC CCGGTCACCTCCTCT <u>CGTGA</u> CCAGGAAAGCCC <u>GGAAATGGGT</u> CATCG AGCTTCAGCCCCATCAAGCCC <u>AAATTGTCG</u>	6457
	CGACAA <u>ATTGGGCTTGA</u> TGGGCTGAAGCTCGATGACCC <u>ATT</u> CGGGCTTCC <u>CTGGTCAAGAGGAGGTGACCGGGGACGACACGGG</u> GAAGAATGCAGAGCTGCAGCGG <u>TAGCCACCAT</u>	6458
	CCTCCTCT <u>CGTGA</u> CCAGGA	6459
	TCCTGGT <u>CAAGAGGAGG</u>	6460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTCCCCGTGTCGCCCCGGTC ACCTCCTCTAGACCATGAAAGCCCGGAAATGGGTATCGAGCTTC AGCCCCATCAAGCCCAAATTGTCGCCAATG	6461
	CATTGGCGACAAATTGGGCTTGATGGGCTGAAGCTCGATGACC CATTCCGGGCTTCATGGTCTAGAGGAGGTGACCGGGACGAC ACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	6462
	CTAGACCATGAAAGCCC	6463
	GGGCTTCATGGTCTAG	6464
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTCCCCGTGTCGCCCCGGTCACC TCCTCTAGACCAAGGGATAGCCCGGAAATGGGTATCGAGCTTCAGC CCCATCAAGCCCAAATTGTCGCCAATGGCG	6465
	CGCCATTGGCGACAAATTGGGCTTGATGGGCTGAAGCTCGATG ACCCATTCCGGGCTATCCTGGTCTAGAGGAGGTGACCGGGAC GACACGGGGAAGAATGCAGAGCTTGCAGCGGT	6466
	GACCAGGATAGCCCAGGA	6467
	TCCGGGCTATCCTGGTC	6468
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly23Term GGA-TGA	GCCACCGCTGCAAGCTCTGCATTCTCCCCCTGCCGTCCCCGGAC ACCTCCTCTAGGCCGTGAAAGCTCGGAAATGGGTATCGAGCTTG AGCCCCCTCAAGCCCAAATTGTCGCCAATG	6469
	CATTGGCGACAAATTGGGCTTGAGGGGGCTAAGCTCGATGACC CATTCCGAGCTTCACGGCCTAGAGGAGGTGCCGGGACGGC AGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	6470
	CTAGGCCGTGAAAGCTC	6471
	GAGCTTCACGGCCTAG	6472
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTCCCCCTGCCGTCCCCGGACACC TCCTCTAGGCCGGGATAGCTCGGAAATGGGTATCGAGCTTGAGC CCCCCTCAAGCCCAAATTGTCGCCAATGCCG	6473
	CGGCATTGGCGACAAATTGGGCTTGAGGGGGCTAAGCTCGAT GACCCATTCCGAGCTATCCGGCCTAGAGGAGGTGCCGGGAC CGGCAGGGGGAAAGAATGCAGAACTTGCAGCGGT	6474
	GGCCGGGATAGCTCGGA	6475
	TCCGAGCTATCCGGCC	6476
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly26Term GGA-TGA	GCAAGTTCTGCATTCTCCCCCTGCCGTCCCCGGACACCTCT AGGCCGGAAAGCTCTGAAATGGGTATCGAGCTTGAGCCCCCT CAAGCCCAAATTGTCGCCAATGCCGGGTTGA	6477
	TCAACCCGGCATTGGCGACAAATTGGGCTTGAGGGGGCTAAGC TCGATGACCCATTCAAGAGCTTCCGGCCTAGAGGAGGTGTCG GGGACGGCAGGGGGAAAGAATGCAGAACTTGC	6478

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAAAGCT <u>T</u> GAAATGGG	6479
	CCC <u>ATTC</u> CAGAGCTTC	6480
5 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Ser29Term TCA-TGA	CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGAA AGCTCGGAAATGGGT <u>G</u> ATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGGTTGAAGGTTAAGGC	6481
	GCCTTAACCTCAACCCGGCATTGGCGACAAATTGGGCTTGAGG GGGCTCAAGCTCGAT <u>C</u> ACCCATTCCGAGCTTCCCAGGCCTAGAG GAGGTGTCGGGGACGGCAGGGGGAAAGAATG	6482
	AAATGGGT <u>G</u> ATCGAGCT	6483
	AGCTCGAT <u>C</u> ACCCATT	6484
	CGTTTAAGTGGATCGGACATTAAAGTGTAAATCATGGTAGCTAT GAGTGCTACTCGCGT <u>A</u> GCTGTTCCGGTTCTTCCCCAAAACCTCA CTCTGGAGCCAAGACATCTGATAAGCTTGG	6485
10 Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Ser9Term TCG-TAG	CCAAGCTTATCAGATGTCTGGCTCCAGAGTGAGGTTTGGGAA GAAACCGGAAACAGCT <u>A</u> CGCAGTAGCACTCATAGCTACCATGATT AAAACACTTAAATGTCGATCCACTTAAACG	6486
	TACTCGCGT <u>A</u> GCTGTTTC	6487
	GAAACAGCT <u>A</u> CGCAGTA	6488
	AGTGTTTAAATCATGGTAGCTATGAGTGCTACTCGCGTGTGTTTC CGGTTTCTTCCCC <u>A</u> ACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTTGCTG	6489
	CAGCAACACTACCTGGTCACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGTT <u>A</u> TGGGGAAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAAACACT	6490
15 Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys17Term AAA-TAA	CTTCCCC <u>A</u> ACCTCAC	6491
	GTGAGGTT <u>A</u> TGGGGAAAG	6492
	ATGGTAGCTATGAGTGCTACTCGCGTGTGTTCCGGTTCTTCCC CAAAACCTCACTCT <u>T</u> GAGCCAAGACATCTGATAAGCTTGAGGTGA ACCAGGTAGTGTTGCTGTGCGCGGAATCA	6493
	TGATTCCCGCGCACAGCAACACTACCTGGTTACCTCCAAGCTTATC AGATGTCTGGCT <u>C</u> AAGAGTGAGGTTTGGGGAAAGAAACCGGAAA CAGCGACGCAGTAGCACTCATAGCTACCAT	6494
	CTCACTCT <u>T</u> GAGCCAAG	6495
20 Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Gly21Term GGA-TGA	CTTGGCT <u>C</u> AAGAGTGAG	6496

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys23Term AAG-TAG	GCTATGAGTGCTACTGCGTCGCTGTTCCGGTTCTTCCCCAAAAC CTCACTCTGGAGCCTAGACATCTGATAAGCTTGGAGGTGAACCAG GTAGTGTGCTGTGCGCGGAATCAAGACAA	6497
	TTGTCTTGTATTCCCGCGCACAGCAACACTACCTGGTTCACCTCCAAG CTTATCAGATGTCTAGGCTCAGAGTGAGGTTTGGGGAAAGAAAC CGGAAACAGCGACGCAGTAGCACTCATAGC	6498
	CTGGAGCCTAGACATCT	6499
	AGATGTCTAGGCTCCAG	6500
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCC CCAGGAGCCTCCCTTAACTGGGAAGTTAGGCAACTGGTCATCG AGTTTGAGCCCTTCTGAAGCCCAAGTCAA	6501
	TTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATGACCAGTTGC CTAACTTCCCAGGTTAAGGGGAGGCTCCTGGGGATGGAACAGGG AAGCATGCAGAACATTGCTGCAGCAGCCACCAT	6502
	CCTCCCTTAACTGGG	6503
	CCCAGGTTAAGGGGAGG	6504
	GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGGAGCC TCCCTAAACCTGGGTAGTTAGGCAACTGGTCATCGAGTTGAGC CCTTCCTTGAAGCCCAAGTCATCCCCAATG CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATG ACCAGTTGCCTAACTACCCAGGTTAGGGGAGGCTCCTGGGGATG GAACAGGGAAGCATGCAGAACATTGCTGCAGC AACCTGGGTAGTTAGGC	6505 6506 6507 6508
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Trp28Term TGG-TGA	TGCATGCTTCCCTGTTCCATCCCCAGGGAGCCTCCCTAAACCTGG GAAGTTAGGCAACTGATCATCGAGTTGAGCCCTTCTGAAGGCC CAAGTCATCCCCAATGGCGGATTCAGGTT	6509
	AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGG GCTCAAACCTCGATGATCAGTTGCCTAACTTCCCAGGTTAGGGGA GGCTCCTGGGGATGGAACAGGGAAGCATGCA	6510
	GGCAACTGATCATCGAG	6511
	CTCGATGATCAGTTGCC	6512
	CATGCTTCCCTGTTCCATCCCCAGGGAGCCTCCCTAAACCTGGGA AGTTAGGCAACTGGTGTATCGAGTTGAGCCCTTCTGAAGCCCA AGTCATCCCCAATGGCGGATTCAGGTTAA TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAA GGGCTCAAACCTCGATCACCAGTTGCCTAACTTCCCAGGTTAGGG GAGGCTCCTGGGGATGGAACAGGGAAGCATG	6513 6514

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO
	CAACTGGT <u>GATCGAGTT</u>	6515
	AACTCGAT <u>CACCAGTTG</u>	6516
5 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys21Term AAA-TAA	ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTCTCCGTTCCAACC CCGGGAATCTCCCCT <u>TAACCCGGGAAGTCGGTAATGGTGGCTT</u> CAGGTTAAGGCAAACGCCAATGCCCATCCTA	6517
	TAGGATGGGCATTGGCGTTGCCTTAACCTGAAAGCCACCATTAC CGAACTTCCC <u>GGGTTAAGGGGAGATTCCC</u> GGGGTTGGAACGGAG AAGAATGCAGAACTTGCTGCCAGCCACCAT	6518
	TCTCCC <u>CTTAACCCGGG</u>	6519
	CCCGGG <u>TTAAGGGGAGA</u>	6520
10 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	GCCGCAGCAAGTTCTGCATTCTCTCCGTTCCAACCCGGGAATC TCCCCTAAACCCGGG <u>TAGTCGGTAATGGTGGCTT</u> CAGGTTAAG GCAAACGCCAATGCCCATCCTAGTCTAAAGT	6521
	ACTTAGACTAGGATGGGCATTGGCGTTGCCTTAACCTGAAAGCC ACCATTACCGAA <u>CTACCCGGGTTAAGGGGAGATTCCC</u> GGGGTTGG AACGGAGAAGAATGCAGAACTTGCTGCC	6522
	AACCCGGG <u>TAGTCGGT</u>	6523
	ACCGAA <u>CTACCCGGGTT</u>	6524
15 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gln31Term CAG-TAG	TTCTCCGTTCCAACCCGGGAATCTCCC <u>CTAAACCCGGGAAGTTC</u> GGTAATGGTGGCTT <u>TTAGGTTAAGGCCAAACGCCAATGCCCATCCT</u> AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	6525
	CTTCAGTCTCGAGGCTGCCAGACTT <u>AGACTAGGATGGCATTGG</u> CGTTTGCC <u>TTAACCTAAAGGCCACCATTACCGAACTTCCC</u> GGGGTT AGGGGAGATTCCC <u>GGGGTTGGAACGGAGAA</u>	6526
	GTGGCT <u>TTTAGGTTAAG</u>	6527
	CTTAAC <u>CTAAAGGCCAC</u>	6528
20 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys33Term AAG-TAG	GTTC <u>CAACCCGGGAATCTCCC</u> CTAAACCCGGGAAGTCGGTAAT GGTGG <u>CTTCAGGTT</u> <u>TTAGGCCAAACGCCAATGCCCATCCTAGTCTA</u> AAGTCTGGCAGCCTCGAGACTGAAGATGACA	6529
	TGT <u>CATCTTCAGTCTCGAGGCTGCCAGACTT</u> <u>AGACTAGGATGGG</u> CATTGGCGTTGC <u>CTAAACCTGAAAGGCCACCATTACCGAACTTCCC</u> GGG <u>TTTAGGGGAGATTCCC</u> GGGGTTGGAAC	6530
	TTCAGG <u>TTTAGGCCAAAC</u>	6531
	GT <u>TTGCCTAAACCTGAA</u>	6532

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Gln21Term CAA-TAA	ATGTTGAAGCTCTCGTGTAAATGCGACTGATAAGTTACAGACCCCTCTCTCGCATTCTCATTAACCGGATCCGGCACACCGGAGAACCGTCTCCGGTCTCCGGTCTCCGGT	6533
	CCTCCGTGTCGTGCTCTCATCTGAGGAAC	
	GTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGTGTGCTCTCATGAGGAATGCGAGAACAGAGGGTCTGTAACAT	6534
	TATCAGTCGATTACACGAGAGCTTCAACAT	
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Arg28Term AGA-TGA	ATTCTCATTAACCGGAT	6535
	ATCCGGTTAATGAGAAT	6536
	GCGACTGATAAGTTACAGACCCCTCTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAC	6537
	ATCCGGCACACCGGTTAATGAGAATGCGAGAACCGGTTCTCCGTGTCGTGCTCTCATCTGAGGAACCCGGTTCTCGATCCTTGCGAG	
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Ser24Term TCG-TAG	CTCGCAAAGGATCGAGAACCGGTTCTCAGATGAGAGCACGACA	6538
	CGGAGGAGACGGTTCAACCGGTTGCGAGAACAGAGGGTCTGTAACTTACAGTCGC	
	CACACCGGTTAACCCTGTC	6539
	GACGGTTCAACCGGTTG	6540
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Ser24Term TCG-TAG	CCCTCTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAA	6541
	CCGTCTCCTCCGTGTAAGTGCTCTCATCTGAGGAACCCGGTTCTCGATCCTTGCGAGCGATCGTATCTGCTGATCA	
	TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTC	6542
	CTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTGTGCGGATCCGGTTGATGAGAACATGCGAGAACAGAGGG	
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Cys25Term TGC-TGA	CTCCGTGTAAGTGCTCTC	6543
	GAGAGCACTACACGGAG	6544
	CTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGT	6545
	CTCCTCCGTGTCGTGATCTCATCTGAGGAACCCGGTTCTCGATCTTGCGAGCGATCGTATCTGCTGATCAAGGA	
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Cys25Term TGC-TGA	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG	6546
	TTTCCTCAGATGAGATCACGACACCGGAGGAGACGGTTCTCCGGTGCGCGGATCCGGTTGATGAGAACATGCGAGAACAG	
	GTGTCGTGATCTCATCT	6547
	AGATGAGATCACGACAC	6548
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG	ATTCTTCTCTATAAACCAAAACCTCAGGAACCATAAAAAAAGGCATCAAAATGTAAGAGCTTCGTGTAAATGTGACTAACAACTTAC	6549
	ACACCTTCTCCTTCTCCGATTCTC	
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG	GAGGAATCGGAGAAGAAGGAGAAGGGTGTGTAAGTTGTTAGTCACATTACATTGATGCCCTTTTTTTATGGTT	6550
	CTGAGGTTTGGTTATAGAAGAAGAAT	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAAATGT <u>AGAAGCTT</u>	6551
	AAAGCTTC <u>TACATTTT</u>	6552
5 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Lys3Term AAG-TAG	TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAGGG CATCAAAAATGTTG <u>TAGCTTCTCGTGTAAATGTGACTAACAACTTACAC</u> ACCTCTCCTCTTCTCCGATTCCCTCCC	6553
	GGGAGGAATCGGAGAAGAAGGGAGAAGGTGTGAAGTTGTTAGTCA CATTACACGAAAGCT <u>ACAACATTTTGATGCCCTTTTTTTATGG</u> TTCCTGAGGTTTGGTTATAGAAGAAGA	6554
	AAATGTTG <u>TAGCTTCTG</u>	6555
	CGAAAGCT <u>ACAACATTT</u>	6556
	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAGGGCATCAA AATGTTGAAGCTT <u>AGTGTAAATGTGACTAACAACTTACACACCTTCT</u> CCTTCTTCTCCGATTCCCTCCCTTTCAT	6557
10 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Ser5Term TCG-TAG	ATGAAAAGGGAGGAATCGGAGAAGAAGGGAGAAGGTGTGAAGTTG TTAGTCACATTACACTAAAGCTTCAACATTTTGATGCCCTTTTT TTATGGTTCTGAGGTTTGGTTATAG	6558
	GAAGCTT <u>AGTGTAAATG</u>	6559
	CATTACACTAAAGCTTC	6560
	AAACCAAAACCTCAGGAACCATAAAAAAAAAGGGCATCAAAATG TTGAAGCTTCTGT <u>GAATGTGACTAACAACTTACACACCTTCTCCTT</u> CTTCTCCGATTCCCTCCCTTTCATCCCG	6561
	CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGGAGAAGGTGTGA AGTTGTTAGTCACATT <u>ICACGAAAGCTTCAACATTTTGATGCCCTT</u> TTTTTTATGGTTCTGAGGTTTGGTT	6562
15 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Cys6Term TGT-TGA	CTTCTGT <u>GAATGTGAC</u>	6563
	GTCACATT <u>ICACGAAAG</u>	6564

**Table 23**  
**Oligonucleotides to produce plants with increased stearate**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCAATTCAATCATATC CAGAAATGGCTCTATAGTTAACCCCTTGGTGGCATCTCAGCCTTA CAAATTCCCTTCCTCGACTCGTCCGCCAA	6565
		TTGGCGGACGAGTCGAGGAAGGAAATTGTAAGGCTGAGATGCCA CCAAAGGGTTAAACTATAGAGCCATTCTGGATATGATGAATGAAT CCTTCTTTCTACAGAGCTAGAGCTCTCCC	6566
		TGGCTCTATAGTTAAC	6567
		GTAAACTATAGAGCCA	6568
10	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGATTCAATTCAATCATATCCAGAAATGGCTCT AAAGTTAACCCCTTAGGTGGCATCTCAGCCTTACAAATTCCCTTCC TCGACTCGTCCGCCAACCTCCTCTTCAG	6569
		CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGAAATTGTA GGCTGAGATGCCACCTAAGGGTTAAACTTAGAGCCATTCTGGAT ATGATGAATGAATCCTCTTTCTACAGAG	6570
		TAACCCTT <del>AGGTGGCAT</del>	6571
		ATGCCACCTAAGGGTTA	6572
		AGAAGGATTCAATTCAATCATATCCAGAAATGGCTCTAAAGTTAAC CTTGGTGGCATCT <del>TAGCCTTACAAATTCCCTCCTCGACTCGTCC GCCAACTCCTCTTCAGATCTCCCAAGT</del>	6573
15	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Gln12Term CAG-TAG	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA GGGAATTGTAAGGCTAAGATGCCACCAAAGGGTTAAACTTAGAG CCATTCTGGATATGATGAATGAATCCTCT	6574
		TGGCATCT <del>TAGCCTTAC</del>	6575
		GTAAGGCTAAGATGCCA	6576
		TCATTCAATCCAGAAATGGCTCTAAAGTTAACCCCTTGGTG GCATCTCAGCCTT <del>AGAAATTCCCTCCTCGACTCGTCCGCCAAC</del> CTTCTTCAGATCTCCCAAGTTCTGC	6577
		GCAGAGGAACCTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG TCGAGGAAAGGAAATTCTAAGGCTGAGATGCCACCAAAGGGTTAA ACTTCTAGAGCCATTCTGGATATGATGAATGA	6578
20	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Phe14Term TAC-TAG	CAGCCTT <del>AGAAATTCCC</del>	6579
		GGGAATTCTAAGGCTG	6580

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAA AAAGAAAATGGCAT <u>AGAAGCTTAACCC</u> TTGGCATCTCAGCCTTAC AAACTCCCTTCCTCGGCTCGTCCGCCAAT	6581
	ATTGGCGGACGAGCCGAGGAAGGGAGTTGTAGGCTGAGATGC CAAAGGGTTAACGCT <u>CTATGCCATT</u> TTCTTTTGATACGAGGTT	6582
	TGATGTTCTTCAGACACGAGCGAGCTCTC AATGGCAT <u>AGAAGCTT</u> A	6583
	TAAGCTT <u>CTATGCCATT</u>	6584
10 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAA AGAAAATGGCATT <u>TTAGGCTTAACCC</u> TTGGCATCTCAGCCTTACAA ACTCCCTTCCTCGGCTCGTCCGCCAATCT	6585
	AGATTGGCGGACGAGCCGAGGAAGGGAGTTGTAGGCTGAGAT GCCAAAGGGTTAACGCT <u>ACAATGCCATT</u> TTCTTTTGATACGAG	6586
	GTTTGATGTTCTTCAGACACGAGCGAGCTC TGGCATT <u>GTAGCTTAA</u> C	6587
	GTTAACGCT <u>ACAATGCCA</u>	6588
15 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu8Term TTG-TAG	TCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATT GAAGCTTAACCC <u>TTAGGCATCTCAGCCTTACAA</u> ACTCCCTTCCTCG GCTCGTCCGCCAATCTACTCTCAGATC	6589
	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTT GTAAGGCTGAGATGC <u>CTAAGGGTTAACGCTTCAATGCCATT</u> TTTCTT TTTTGATACGAGGTTGATGTTCTTCAGA	6590
	TAACC <u>CTTAGGCATCTC</u>	6591
	GAGATGC <u>CTAAGGGTTA</u>	6592
20 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Gln11Term CAG-TAG	AACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATT <u>GAAGCTTAA</u> CCCTTG <u>GCATCTT</u> AGCCTTACAAACTCCCTCCTCGGCTCGTCCG CCAATCTACTCTCAGATCTCCAA <u>GT</u>	6593
	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA GGGAGTTGTAAGG <u>CTAAGATGCCAAAGGGTTAACGCTTCAATGCC</u> ATTTCTTTTGATACGAGGTTGATGTT	6594
	TGGCAT <u>CTT</u> AGCCTTAC	6595
	GTAAGG <u>CTAAGATGCCA</u>	6596
25 Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln27Term CAA-TAA	AACCAAAAGAAAAAGGTAAAGAAAAAAACAATGGCTCTCAAGCTCA ATCCTTCC <u>TTCTT</u> AAACCCAAAGTTACCTTCTT <u>CGCTCTTCCA</u> CCAATGGCCAGTACCAGATCTCTAA <u>GT</u>	6597
	ACTTAGGAGATCTGGTACTGGCCATTGGTGGAAAGAGCGAAAGAAG GTA <u>ACTTTGGGTTAAGAAAGGAAAGGATTGAGCTT</u> GAGAGCCAT TGTTTCTTAC <u>CTTACCTTTCTTGGTT</u>	6598

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCCTTCT <u>AAACCCAA</u>	6599
	TTGGGTT <u>AAGAAAGGA</u>	6600
Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln29Term CAA-TAA	AAGAAAAAGGTAAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTT TCCTTCTCAA <u>ACCTAAAGTTACCTTTCGCTCTTCCACCAATG</u> GCCAGTACCA <u>GATCTCCTAAGTTCTAC</u>	6601
	TGTAGAA <u>CTTAGGAGATCTGGTACTGGCATTGGTGGAAAGAGCGA</u> AAGAAGGTAA <u>CTTTAGGTTGAGAAAGGAAAGGATTGAGCTTGAG</u> AGCCATTGTTTTTTCTTACCTTTTCTT	6602
	CTCAA <u>ACCTAAAGTTA</u>	6603
	TAAC <u>TTAGGTTGAG</u>	6604
Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys30Term AAG-TAG	AAAAAGGTAA <u>AGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTCC</u> TTTCTCAA <u>ACCCAA<u>ATAGTTACCTTTCGCTCTTCCACCAATGGC</u></u> CAGTACCA <u>GATCTCCTAAGTTCTACATGG</u>	6605
	CCATGTAGAA <u>CTTAGGAGATCTGGTACTGGCATTGGTGGAAAGAG</u> CGAAAGAAGGTAA <u>CTATTGGTTGAGAAAGGAAAGGATTGAGCT</u> TGAGAGCCATTGTTTTTCTTACCTTTT	6606
	AAACCCAA <u>ATAGTTACCT</u>	6607
	AGGTAA <u>CTATTGGTTT</u>	6608
Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys46Term AAG-TAG	TCTCAA <u>ACCCAAAGTTACCTTTCGCTCTTCCACCAATGGCCA</u> GTACCAGAT <u>CTCCTT<u>AGTTCTACATGGCCTCTACCCCTCAAGTCTGG</u></u> TTCTAAGGA <u>AGTTGAGAATCTCAAGAACG</u>	6609
	GCTCTTGAGATT <u>CTCAACTCCTTAGAACCA<u>AGACTTGAGGGTAGA</u></u> GGCCATGTAGAA <u>CTAAGGAGATCTGGTACTGGCATTGGTGGAAAG</u> AGCGAAAGAAGGTAA <u>CTTTGGTTGAGA</u>	6610
	GAT <u>CTCCTT<u>AGTTCTAC</u></u>	6611
	GTAGAA <u>CTAAGGAGATC</u>	6612
Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln11Term CAA-TAA	TCTTCTGATT <u>CAATTAA<u>ACTCATCAATGGCTCTGAGACTGAA</u></u> CCCTAT <u>CCCCAC<u>CTAAAC<u>CTTCTCCCTCCCCAA<u>ATGCCAGTCT</u></u></u> CAGAT<u>CTCCCA<u>GGTTCCG<u>CATGGCCT<u>CTA</u></u></u></u></u>	6613
	TAGAGGCCAT <u>GC<u>GGAA<u>ACCTGG<u>GAGATCTGAGACTGGCATT<u>GG</u></u></u></u> GGGAGGGAGA<u>AGGTT<u>AGGTGGGG<u>ATAGGGTT<u>CAGTCT<u>CAGAGC</u></u></u></u> CATTGAT<u>GAGTAA<u>AGATTAA<u>ATGA<u>ATCAGA<u>AGA</u></u></u></u></u></u></u>	6614
	TCCCCAC <u>CTAA<u>AC<u>CTTC</u></u></u>	6615
	GAAGGTT <u>AGGTGGGG</u>	6616

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln17Term CAA-TAA	CTTACTCATCAATGGCTCTGAGACTGAACCCATCCCCACCCAAA CCTTCTCCCTCCCC <u>T</u> AAATGCCAGTCTCAGATCTCCAGGTTCC GCATGGCCTCTACCCCTCCGCTCCGGTTCCA	6617
	TGGACCCGGAGCGGAGGGTAGAGGCCATGCCAACCTGGGAGAT CTGAGACTGCCATT <u>T</u> AGGGGAGGGAGAAGGTTGGGTGGGGAT AGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG	6618
	CCCTCCCC <u>T</u> AAATGCC	6619
	GCCATT <u>T</u> AGGGAGGG	6620
10 Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Arg22Term AGA-TGA	GCTCTGAGACTGAACCCATCCCCACCCAAACCTTCTCCCTCCCC CAAATGCCAGTCT <u>T</u> GATCTCCAGGTTCCGCATGCCCTTACCC CTCCGCTCCGGTTCCAAAGAGGGTTGAAAATA	6621
	TATTTAACCTCT <u>T</u> GGAACCGGAGCGGAGGGTAGAGGCCATGC GGAACCTGGGAGAT <u>C</u> AGAGACTGCCATTGGGGAGGGAGAAG GTTTGGGTGGGGATAGGGTTCAAGTCTCAGAGC	6622
	CCAGTCT <u>T</u> GATCTCCC	6623
	GGGAGAT <u>C</u> AGAGACTGG	6624
	CAAATGCCAGTCTCAGATCTCCAGGTTCCGCATGCCCTTACCC CTCCGCTCCGGTT <u>C</u> TAAGAGGGTTGAAAATATTAAGAACCCATTCA CTCCTCCCAGAGAACGATGCATGTTCAAGTAA	6625
15 Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Lys37Term AAA-TAA	TTACTTGAACATGC <u>ACT</u> CTCTGGGAGGGAGTGAATGGCTTCTTAAT ATTTTCAACCTCT <u>T</u> AGGAACCGGAGCGGAGGGTAGAGGCCATGCG GAACCTGGGAGAT <u>T</u> GAGACTGCCATTG	6626
	CCGGTT <u>C</u> TAAGAGGGT	6627
	AACCTCT <u>T</u> AGGAACCGG	6628
	CAACAAGCACACACAAGAACAA <u>C</u> ATCAACAA <u>T</u> GGCGATT <u>C</u> GCATCA ATACGGCGACGTT <u>T</u> AA <u>T</u> TCAGACCTGTACCGTT <u>C</u> ATT <u>C</u> GC <u>T</u> TTCC TCAACCGAAAC <u>C</u> TC <u>T</u> CA <u>G</u> AT <u>C</u> CC <u>A</u> AT	6629
20 <i>Helianthus annuus</i> Gln11Term CAA-TAA	ATTGGGAGAT <u>T</u> GAGAGGTT <u>C</u> GG <u>T</u> GAG <u>A</u> AC <u>C</u> GA <u>A</u> TC <u>A</u> GGTACAGGTCT <u>G</u> ATT <u>A</u> AA <u>C</u> GT <u>C</u> GC <u>C</u> GT <u>T</u> GT <u>G</u> CT <u>T</u> GT <u>T</u> TT <u>G</u> TT <u>G</u> AT <u>G</u> TT <u>G</u> TT <u>C</u> TT <u>G</u> T <u>G</u> CT <u>G</u> TT <u>G</u> TT <u>G</u>	6630
	CGACGTT <u>T</u> AA <u>T</u> CAGAC	6631
	GT <u>T</u> GT <u>G</u> ATT <u>A</u> AA <u>C</u> GT <u>C</u> G	6632
	AAGCACACACAAGAAC <u>C</u> ATCAACAA <u>T</u> GGCGATT <u>C</u> GCATCA <u>A</u> GGCGACGTT <u>C</u> AA <u>T</u> <u>G</u> AGAC <u>C</u> GT <u>T</u> AC <u>C</u> CG <u>T</u> <u>T</u> <u>C</u> ATT <u>C</u> GC <u>T</u> TT <u>C</u> CT <u>C</u> AA CCGAAAC <u>C</u> TC <u>T</u> CA <u>G</u> AT <u>C</u> CC <u>A</u> ATT <u>C</u> GC	6633
25 <i>Helianthus annuus</i> Ser12Term TCA-TGA	GCGAATTGGGAGAT <u>T</u> GAGAGGTT <u>C</u> GG <u>T</u> GAG <u>A</u> AC <u>C</u> GA <u>A</u> TC <u>A</u> GAACGGTACAGGT <u>T</u> <u>C</u> ATT <u>G</u> AA <u>A</u> CG <u>T</u> CG <u>C</u> CG <u>T</u> <u>T</u> GT <u>G</u> CT <u>T</u> GT <u>G</u> CT <u>T</u>	6634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTTCAAT <u>GAGACCTGT</u>	6635
	ACAGGTCT <u>CATTGAAAC</u>	6636
5 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAC-TAG	AAGAACAAACATCAACAATGGCGATTCGCATCAATAACGGCGACGTTT CAATCAGACCTGT <u>A<u>CGTT</u>CATT<u>CGCGTT</u>CCTCAACCGAAACCTC</u> TCAGATCTCCCAAATT <u>CGCCATGGCTT</u> CC	6637
	GGAAGCCATGGCGAATTGGGAGATCTGAGAGGTT <u>CGGTT</u> GAGG AAACCGGAAT <u>GAACG</u> <u>CTACAGGT</u> CTGATT <u>GAAACGT</u> CGCCGTATT	6638
	GACCTGT <u>AGCGTT</u> CATT	6639
	AATGAAC <u>CG</u> <u>CTACAGGT</u> C	6640
	CAACATCAACAATGGCGATT <u>CGCATCAATAACGGCGACGTT</u> CAATC AGACCTGT <u>ACCGTT</u> GATT <u>CGCGTT</u> CCTCAACCGAAACCTCTCAGA TCTCCCAAATT <u>CGCCATGGCTT</u> CCACCAT	6641
10 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser17Term TCA-TGA	ATGGTGGAGCCATGGCGAATTGGGAGATCTGAGAGGTT <u>CGGT</u> TGAGGAAACCGGAAT <u>CAACGG</u> TACAGGTCTGATT <u>GAAACGT</u> CGCC GTATTGAT <u>CGCAATGCCATTGTTGATGTTG</u>	6642
	GTACCGTT <u>GATT</u> CGCGT	6643
	ACCGGAAT <u>CAACGG</u> TAC	6644
	ACACACAAACACACACTCAATCACACACACATCATCTTCTTCATC AACGATGGCGTT <u>I</u> GAATGAGTCCGGTGACGCTTCAACGGGAGAT ATATCCTTCATA <u>ACACT</u> TT <u>TCATCAATCGA</u>	6645
	TCGATTGAT <u>AAAAGT</u> GTAT <u>GAAGG</u> ATAT <u>CTCCGTT</u> GAAGCGT CACCGGACTCATT <u>CAAAAGGCCATCGTT</u> GAT <u>GAAGAAG</u> ATGATGA TGTGTGTGATT <u>GAGTGTGTTGTTG</u>	6646
15 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Arg4Term CGA-TGA	TGGCGCTT <u>I</u> GAAT <u>GAGT</u> ACTCATT <u>CAAAAGGCCA</u>	6647 6648
	ACACACACATCATCATCTTCTTCATCAACGATGGCGCTT <u>CGAATGA</u> GTCCGGTGACGCTT <u>I</u> AACGGGAGATAT <u>TCCTTCATACACT</u> TTCA TCAAT <u>CGAAAAAT</u> TCAGAT <u>CTCCTAAAT</u>	6649
	ATTTAGGAGAT <u>CTGAGA</u> TT <u>TCGATTGATGAAAGTGTATGAAGG</u> ATATAT <u>CTCCGTT</u> <u>AAAGCGTCACCGGACTCATT</u> GAAGCGCCAT CGTTGAT <u>GAAGAAG</u> ATGATGATGTGTTG	6650
	TGACGCTT <u>AAACGGGAG</u>	6651
	CTCCCGTT <u>AAAGCGTCA</u>	6652
20 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTCGAATGAGTCCGG TGACGCTTCAACGG <u>T</u> AGATATATCCTTCATACACTTTCATCAATCG AAAAATCTCAGATCTCCTAAATTGCGCA	6653
		TCGCGAATTAGGAGATCTGAGATTTTCGATTGATGAAAAGTGT TGAAGGATATATCT <u>ACCGTTGAAGCGTCACCGGACTCATTGAA</u> CGCCATCGTTGATGAAGAAGATGATGATGT	6654
		TTCAACGG <u>T</u> AGATATAT	6655
		ATATATCT <u>ACCGTTGAA</u>	6656
		ATCTTCTTCATCAACGATGGCGCTCGAATGAGTCCGGTGACGCTT CAACGGGAGATATAG <u>C</u> CTTCATACACTTTCATCAATCGAAAATCT CAGATCTCCTAAATTGCGATGGCTTCC	6657
10	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAT-TAG	GGAAGCCATCGCGAATTAGGAGATCTGAGATTTTCGATTGATGA AAAGTGTATGAAGG <u>C</u> TATATCTCCCGTTGAAGCGTCACCGGACTC ATTGAAGCGCCATCGTTGATGAAGAAGAT	6658
		GAGATATAG <u>C</u> CTTCATA	6659
		TATGAAGG <u>C</u> TATATCTC	6660
		AACTCAGCCAGCTGCCCAAAACAACAGCGCAGAAAAACCTCA ACAACAATGGCTCT <u>T</u> AGCTCAACCCAGTCACCACCTCCCTCAA CACGCTCCCTCAACA <u>ACTTCTCCTCCAGAT</u>	6661
		ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTGAAGGGAAGGTG GTGACTGGGTTGAG <u>C</u> TAGAGAGCCATTGTTGTTGAAGGTTTCTG CGCTGTTTTGGGGCAAGCTGGCTGAGTT	6662
15	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys4Term AAG-TAG	TGGCTCT <u>T</u> AGCTCAAC	6663
		GTTGAG <u>C</u> TAGAGAGCCA	6664
		GCGCAGAAAAACCTCAACAACAATGGCTCTAACGCTAACCCAG TCACCACCTCCCT <u>G</u> AACACGCTCCCTAACAA <u>CTTCTCCTCCAG</u> ATCTCCTCGCAC <u>TTCTCATGGCTGCTTC</u>	6665
		GAAGCAGCCATGAGAAAGGTGCAGGGAGATCTGGAGGAGAAGTT GTTGAGGGAGCGTGT <u>C</u> AAGGGAGGTGGTACTGGGTTGAGCT TGAGAGCCATTGTTGTTGAAGGTTTCTGCGC	6666
		CTTCCCT <u>G</u> AACACGCT	6667
20	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Ser13Term TCA-TGA	AGCGTGT <u>T</u> CAAGGGAG	6668
		CTCAAGCTAAC <u>CCAGTCACCACCTCCCTAACACACGCTCCCTC</u> AACAA <u>CTTCTCCTCCTGATCTCCTCGCAC</u> CTTCTCATGGCTGCTT CCACTTCAATT <u>CCACCTCCACCAAGTAAG</u>	6669
		CTTACTTGGTGGAGGTGGAATTGAAAGTGGAGCAGCCATGAGAA AGGTGCGAGGAGAT <u>C</u> AGGAGGAGAAGTTGTTGAGGGAGCGTGT GAAGGGAGGTGGTACTGGTTGAGCTTGTGAG	6670
25	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Arg23Term AGA-TGA		
30	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Arg23Term AGA-TGA		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCTCCTCC <u>T</u> GATCTCCT	6671
	AGGAGAT <u>C</u> AGGAGGAGA	6672
Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys41Term AAG-TAG	TCCCTCCAGATCTCCTCGCACCTTCTCATGGCTGCTTCCACTTTCA ATTCCACCTCCAC <u>C</u> AGTAAGCATCTCCTCCTCGGAATCTCG CCGATTCTTTAAGCGATTGATCGTAGA	6673
	TCTACGATCAATCGCTAAAGAAATCGGCGGAGATTCCGAGGAG GAGGAGATGCTTACT <u>A</u> GGTGGAGGTGGATTGAAAGTGGAAAGCAG CCATGAGAAAGGTGCGAGGAGATCTGGAGGA	6674
	CCTCCAC <u>C</u> AGTAAGCA	6675
	TGCTTACT <u>A</u> GGTGGAGG	6676
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Arg21Term AGA-TGA	ATGGCACTGAAACTTGCCTCCACCCCCACAAGATGCCCTCCCTCC CCGATGCTCGTAT <u>C</u> GATCTCACAGGGTTTCATGGCTCAACTAT TCATTCTCCTCTATGGAGGTGGAAAAG	6677
	CTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCCCTGTGAGAT <u>C</u> AGATACGAGCATCGGGGAAGGAAGGCATCTT GTGGGGTGGAAAGCAAAGTTCAAGTGCATGCCAT	6678
	CTCGTAT <u>C</u> GATCTCAC	6679
	GTGAGAT <u>C</u> AGATACGAG	6680
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Ser29Term TCA-TGA	CCCACAAGATGCCCTCCCTCCCCGATGCTCGTATCAGATCTCAC GGGTTTCATGGCTT <u>G</u> AACTATTCTACAGGCCTCCACG AAAAGTTAAAAGCCTTCACGCCCTCACG	6681
	CGTGGAGGCGTAAAGGCTTTAACTTTCCGACCTCCATAGAAG GAGAATGAATAGTT <u>C</u> AAGCCATGAAAACCCCTGTGAGATCTGATACG AGCATCGGGGAAGGAAGGCATCTGTGGG	6682
	CATGGCTT <u>G</u> AACTATT	6683
	GAATAGTT <u>C</u> AAGCCATG	6684
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Glu37Term GAG-TAG	GATGCTCGTATCAGATCTCACAGGGTTTCATGGCTCAACTATT ATTCTCCTCTAT <u>G</u> AGGTGGAAAAGTTAAAAGCCTTCACGCC TCCACGAGAGGTACATGTTCAAGTAACCC	6685
	GGGTTACTTGAACATGTACCTCTCGTGGAGGC <u>G</u> TGAAAGGCTTT AACTTTCCGAC <u>C</u> ATAGAAGGAGAATGAATAGTTGAAGCCATG AAAACCC <u>T</u> GTGAGATCTGATACGAGCATC	6686
	CTTCTAT <u>G</u> AGGTGGGA	6687
	TCCGAC <u>C</u> ATAGAAG	6688

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTATGGCTTCAACTATTCTTCAG CTTCTATGGAGGT <u>T</u> GAAAAGTTAAAAGCCTTCACGCCTCCACG AGAGGTACATGTTCAAGTAACCCATTCT	6689
	AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGC <u>G</u> TGAAAG GCTTTTTAAC <u>T</u> TC <u>A</u> GACCTCCATAGAAGGAGAATGAATAGTTGA AGCCATGAAAACCTGTGAGATCTGATACG	6690
	TGGAGGT <u>T</u> GAAAAGTT	6691
	AACTTT <u>C</u> AGACCTCCA	6692
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys4Term AAA-TAA	TTCTCGTTTGTGCGCCCCCTGCTCTCTCTCTATCAGGCACG GAGAAATGGCACT <u>T</u> GA <u>CT</u> CA <u>CT</u> CCAGTCATGTTCAATCTCAGAA GCTTCCATTCTGCCTCCTATCCGCCTT	6693
	AAGGCGGATAGGAGGCAAGAAATGGAAGCTCTGAGATTGAAACA TGACTGGACTGAGTT <u>A</u> CGTGC <u>CA</u> TTCTCCGTGCCTGATAGAGA GAGAGAGCAGAGGGACGACAAAAACGAGAA	6694
	TGGCACT <u>T</u> GA <u>CT</u> CA <u>GT</u> GCCA	6695
	ACTGAGTT <u>A</u> CGTGC <u>CA</u>	6696
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln11Term CAA-TAA	CTGCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTC AGTCCAGTCATGTT <u>T</u> AATCTCAGAAGCTCCATTCTGCCTCCTA TCCGCCTCCAATCTCAGATCTCCGAGGG	6697
	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT GGAAGCTCTGAGATT <u>AA</u> ACATGACTGGACTGAGTT <u>C</u> AGTGCC <u>A</u> TTTCTCCGTGCCTGATAGAGAGAGAGAGCAG	6698
	TCATGTT <u>T</u> AATCTCAG	6699
	CTGAGATT <u>AA</u> ACATGA	6700
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln13Term CAG-TAG	TCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA GTCATGTT <u>C</u> AA <u>CT</u> <u>T</u> AGAAGCTCCATTCTGCCTCCTATCCGC CTT <u>CC</u> AA <u>CT</u> TCAGATCTCCGAGGGTTT <u>C</u> A	6701
	TGAAAAC <u>CC</u> CTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA GAAATGGAAGCT <u>T</u> <u>C</u> <u>A</u> AGATTGAAACATGACTGGACTGAGTT <u>C</u> TGCCATTCTCCGTGCCTGATAGAGAGAGA	6702
	TT <u>CA</u> AT <u>CT</u> <u>T</u> AGAAGCTT	6703
	AAGCT <u>T</u> <u>C</u> <u>T</u> <u>A</u> AGATTGAA	6704
Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys14Term AAG-TAG	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC ATGTT <u>CC</u> AA <u>CT</u> TCAG <u>T</u> AGCT <u>CC</u> ATTCTGCCTCCTATCCGCCTC CAAT <u>CT</u> CA <u>GT</u> ATCTCCGAGGGTTT <u>C</u> ATGG	6705
	CCATGAAAAC <u>CC</u> CTCGGAGATCTGAGATTGGAAGGCGGATAGGAGG CAAGAAATGGAAG <u>C</u> <u>T</u> <u>A</u> CTGAGATTGAAACATGACTGGACTGAGTT CA <u>GT</u> GCCATTCTCCGTGCCTGATAGAGAG	6706

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	AATCTCAG <u>T</u> AGCTTCCA	6707
	TGGAAG <u>C</u> T <u>A</u> CTGAGATT	6708
5 Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Tyr12Term TAC-TAG	CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTGGCGGCGTCCC ACACCGCATGCCGTAG <u>T</u> CTGCCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCGAAGATGGTGGCCATGGCC	6709
	GGCCATGGCCACC <u>A</u> CTTCGACATCCCATTGCTCCTCTGCGC CACGCCGGCGCAG <u>G</u> ACTACGGCGATGCGGTGCGGACGCCGCG AACGCCATGAGCAGCGCAGCGAGATCTGGGG	6710
	TCGCCGTAG <u>T</u> CTGCGG	6711
	CCGCAGG <u>A</u> CTACGGCGA	6712
	CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATGCCGTACTC CTGCGGCGGCGTGGCGTAGAGGAGGAGCAATGGGATGTCGAAGA TGGTGGCCATGGCCTCCACC <u>A</u> CACAGGGTCA	6713
10 Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Gln19Term CAG-TAG	TGACCCTGTTGATGGTGGAGGCCATGCCACC <u>A</u> CTTCGACATCC CATTGCTCCTCT <u>A</u> CGCCACGCCCGCAGGAGTACGGCGAT GCGGTGTGGACGCCCGAACGCCATGAGCAG GCGTGGCG <u>T</u> AGAGGAGG	6714
	CCTCCT <u>T</u> ACGCCACGC	6715
	CCCACACCGCATGCCGTACTCCTGCCGGCGTGGCGCAGAG GAGGAGCAATGGGATGT <u>A</u> GAAGATGGTGGCCATGGCCTCCACCA TCAACAGGGTCAAGACTGCTAAGAACGCCCTACAC	6716
	GTGTAGGGCTTCTTAGCAGTCTGACCC <u>T</u> GTGATGGTGGAGGCC ATGGCCACC <u>A</u> CTCCATTGCTCCTCTGCGCCACG CCGCCGAGGAGTACGGCGATGCGGTGTGGG	6717
	TGGGATGT <u>A</u> GAAGATGG	6718
15 Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Ser26Term TCG-TAG	CCATCTT <u>T</u> ACATCCC	6719
	CACACCGCATGCCGTACTCCTGCCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCG <u>T</u> AGATGGTGGCCATGGCCTCCACC <u>A</u> AA CAGGGTCAAGACTGCTAAGAACGCCCTACACTC	6720
	GAGTGTAGGGCTTCTTAGCAGTCTGACCC <u>T</u> GTGATGGTGGAGG CCATGGCCACC <u>A</u> CTACGACATCCCATTGCTCCTCTGCGCCA CGCCGCCGAGGAGTACGGCGATGCGGTGTG	6721
	GGATGTCG <u>T</u> AGATGGTG	6722
	CACCAT <u>T</u> ACGACATCC	6723
20 Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Lys27Term AAG-TAG	6724	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Leu3Term TTG-TAG	TTCTCTCTAGGTTGAGCGGTACCAACAGAACACTTAGGAGA GAGAAGCAATGGCGT <del>A</del> GAAGCTTACCCACACGGCCTCAATCCT CCATGGCGGTTACCTCTCGGGACTCCTCG	6725
		CGAGGAAGTCCCAGAGAGGTAAACGCCATGGAAGGATTGAAGGC CGTGTGGTGAAGCTT <del>C</del> ACGCCATTGCTTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTAACCTAGAGAGAGAA	6726
		AATGGCGT <del>A</del> GAAGCTTC	6727
		GAAGCTT <del>C</del> ACGCCATT	6728
		CTCTCTCTAGGTTGAGCGGTACCAACAGAACACTTAGGAGAGA GAAGCAATGGCGTT <del>G</del> AGCTTACCCACACGGCCTCAATCCT ATGGCGGTTACCTCTCGGGACTCCTCGAT	6729
10	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Lys4Term AAG-TAG	ATCGAGGAAGTCCCAGAGAGGTAAACGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCT <del>A</del> CAACGCCATTGCTTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTAACCTAGAGAGAG	6730
		TGGCGTT <del>G</del> AGCTTCAC	6731
		GTGAAGCT <del>A</del> CAACGCCA	6732
		AAGCAATGGCGTTGAAGCTTACCCACACGGCCTCAATCCTCCAT GGCGGTTACCTCT <del>T</del> AGGGACTCCTCGATCGTATCACCTCAGATC TCACCGCGTTTCATGGCTTCTTACAAT	6733
		ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATAC GATCGAGGAAGTCC <del>T</del> AAAGAGGTAAACGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTTCAACGCCATTGCTT	6734
15	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Ser19Term TCG-TAG	TACCTCT <del>T</del> AGGGACTTC	6735
		GAAGTCCC <del>T</del> AAAGAGGTAA	6736
		GCAATGGCGTTGAAGCTTACCCACACGGCCTCAATCCTCCATG GCGGTTACCTCTCGT <del>G</del> ACTCCTCGATCGTATCACCTCAGATCTC ACCGCGTTTCATGGCTTCTTACAATTG	6737
		CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGAT ACGATCGAGGAAGTC <del>A</del> CGAAGAGGTAAACGCCATGGAAGGATTGA AGGCCGTGTGGTGAAGCTTCAACGCCATTGCTT	6738
		CCTCTT <del>CGT</del> AGCTTCCT	6739
20	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Gly20Term GGA-TGA	AGGAAGTC <del>A</del> CGAAGAGGTAA	6740
		TGGCTCTGAATCTCAACCCCGTTCCACACCAATT <del>C</del> AGTGT <del>C</del> TCG ATTGCCGT <del>CTT</del> CT <del>G</del> ACCTCGTCAAACGCC <del>T</del> TC <del>G</del> CAGATCTCCC AAATTCTTCATGGCTTCCACTCTCAGCAG	6741
		CTGCTGAGAGTGGAGGCCATGAAGAATTGGGAGATCTGCGAGAA GGCGTTGACGAGGT <del>C</del> AGAAAGACGGCAATCGACGACACTGAAAT GGTGTGAAACGGGTTGAGATT <del>C</del> AGAGCCA	6742
25	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Ser21Term TCA-TGA		
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTCTTCT <u>GACCTCGTC</u>	6743
	GACGAGGT <u>CAGAAAGAC</u>	6744
5 Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Gln24Term CAA-TAA	AATCTCAACCCGTTCCACACCATT <u>CAGTGTGTCGATTGCCGT</u> CTTCTCACCTCGT <u>AAACGCCCTCTCGCAGATCTCCCAAATTCTT</u> CATGGCTTCCACTCT <u>CAGCAGCTCTTCTC</u>	6745
	GAGAAGAGCTGCT <u>GAGAGTGGAAAGCCATGAAGAATTGGGAGATC</u> TGC <u>GAGAAGGC</u> GT <u>TAACGAGGTGAGAAAGACGGCAATCGACGA</u> CACTGAA <u>ATGGTGTGGAAACGGGTTGAGATT</u>	6746
	<u>CACCTCGT</u> <u>AAACGCCT</u>	6747
	AGGC <u>GTTAACGAGGTG</u>	6748
	TCCACACCATT <u>CAGTGTGTCGATTGCCGT</u> <u>CTTCTCACCTCGTC</u> AAACGCCT <u>CTCGCTGATCTCCCAAATTCTT</u> <u>CATGGCTTCCACTCT</u> CAGCAGCT <u>CTTCTCCTAAGGAAGCGGAA</u>	6749
10 Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Arg29Term AGA-TGA	TTTCCGCT <u>CTCTAGGAGAAAGAGCTGCTGAGAGTGGAAAGCCATGA</u> AGA <u>ATTGGGAGATCAGCGAGAAGGC</u> GT <u>TTGACGAGGTGAGAAAG</u> ACGGCA <u>ATCGACGACACTGAAATGGTGTGGA</u>	6750
	<u>CTTCTCGCTGATCTCCC</u>	6751
	GGGAGAT <u>CAGCGAGAAG</u>	6752
	TTTCAGTGT <u>CGTCGATTGCCGT</u> <u>CTTCTCACCTCGT</u> <u>CAAACGCC</u> TT CTCGCAGAT <u>CTCCCTAATTCTT</u> <u>CATGGCTTCCACTCTCAGCAGCTC</u> <u>TTCTCCTAAGGAAGCGGAAAGCCTGAAGA</u>	6753
15 Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Lys32Term AAA-TAA	TCTTCAGG <u>CTTCCGCT</u> <u>CTCTAGGAGAAAGAGCTGCTGAGAGTGG</u> AAGCCAT <u>GAAGAATTAGGGAGATCTGCGAGAAGGC</u> GT <u>TTGACGAG</u> GT <u>GAGAAAGACGGCAATCGACGACACTGAAA</u>	6754
	<u>GATCTCCCTAATTCTTC</u>	6755
	GAAGAATT <u>AGGGAGATC</u>	6756
	AAATAGTC <u>GAGGTGAAAAACAGAGCATCAACAA</u> TGGCA <u>CTGAATAT</u> CAATGGGGTGT <u>CGT</u> <u>GAAAATCTCACAA</u> ATGTT <u>ACCATT</u> <u>CCCTTG</u> T	6757
	TCTTCAG <u>CCAGATCTGAGCGAG</u> TTTCAT AT <u>GAAAATCGCTCAGATCTGGCTGAAGAACAGGAAATGGTAACA</u> TTTGT <u>GAGATTTCACGACACCCATTGATATT</u> <u>CAGTGCCATTGTT</u> GAT <u>GCTCTGTTTCACCTCGACTATT</u>	6758
20 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu10Term TTA-TGA	GGTGT <u>CGT</u> <u>GAAAATCTC</u>	6759
	GAGATT <u>TTCACGACACC</u>	6760

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCA ATGGGGTGTGCGTTATAATCTCACAAAATGTTACCATTCCTGTTCT TCAGCCAGATCTGAGCGAGTTTCATGG	6761
	CCATGAAAACTCGCTCAGATCTGGCTGAAGAACAGGAAATGGTA ACATTTGTGAGATTATAACGACACCCCATTGATATTCACTGCCATT GTTGATGCTCTGTTTACCTCGACTAT	6762
	TGTGTTATAATCTCAC	6763
	GTGAGATTATAACGACA	6764
10 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys14Term AAA-TAA	GTGAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGT CGTTAAAATCTCACATAATGTTACCATTCCTGTTCTCAGCCAGA TCTGAGCGAGTTTCATGGCTTCAACCA	6765
	TGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAG GAAATGGTAACATTAGTGAGATTATAACGACACCCCATTGATATT AGTGCCATTGTTGATGCTCTGTTTAC	6766
	AATCTCACATAATGTTA	6767
	TAACATTAGTGAGATT	6768
	ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTGTTAAA ATCTCACAAAATGTGACCATTCCTGTTCTCAGCCAGATCTGAG CGAGTTTCATGGCTTCAACCATTATCG	6769
15 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu16Term TTA-TGA	CGATGAATGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAA GAACAAGGAAATGGTCACATTGTTGAGATTATAACGACACCCCATT TGATATTCACTGCCATTGTTGATGCTCTGT	6770
	CAAAATGTGACCATTTTC	6771
	GAAATGGTCACATTG	6772
	TGGCTCTGAGGCTGAACCCCTAACCCCTCACAGAAGCTTTCTCTC TCCTTCTTCATCATGATCTTCTTCTTCATCGTTCTCGCTTCTC AAATGGCTAGCCTCAGATCTCCAAGGTT	6773
20 Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser21Term TCA-TGA	AACCTGGAGATCTGAGGCTAGCCATTGAGGAAGCGAGAACGAT GAAGAAGAAGAAGATCATGATGAAGAAGGAGAGAGAAAGAGCTTC TGTGAAGGGTTAGGGTTAGCCTCAGCCTCAGAGCCA	6774
	TTCATCATGATCTTCTT	6775
	AAGAAGATCATGATGAA	6776
	ACCCTAACCCCTTACAGAAGCTTTCTCTCCCTTCTCATCATCA TCTTCTTCTTCTTGATCGTTCTCGCTTCTCAAATGGCTAGCCTCA GATCTCCAAGGTTCCGCATGGCCTCCAC	6777
25 Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser26Term TCA-TGA	GTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTGA GGAAGCGAGAACGATCAAGAAGAAGATGATGATGAAGAAGGA	6778
	GAGAGAAAGAGCTTGTGAAGGGTTAGGGT	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TTCTTCTT <u>GATCGTTCT</u>	6779
	AGAACGAT <u>CAAGAAGAA</u>	6780
Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser27Term TCG-TAG	CTAACCCCTCACAGAACGCTCTTCTCTCCTCTTCATCATCATCTCTTCTTCAT <u>AGTTCTCGCTCCTCAAATGGCTAGCCTCAGAT</u> CTCCAAGGTTCCGCATGGCCTCCACCCCT AGGGTGGAGGCCATCGGAAACCTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAACTATGAAGAAGAAGAAGATGATGATGAAGA AGGAGAGAGAAAGAGCTTCTGTGAAGGGTAG	6781
	TTCTTCT <u>CAAGAAGAA</u>	6782
	TTCTTCT <u>CAAGAAGAA</u>	6783
	GCGAGAACTATGAAGAA	6784
Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser29Term TCG-TAG	CTTCACAGAACGCTCTCTCTCCTCTTCATCATCATCATCTTCTTCT TCTTCATCGTT <u>CAAGAAGAA</u> CTCAAATGGCTAGCCTCAGATCTCCAA GGTTCCGCATGGCCTCCACCCCTCCGCAC GTGCGGAGGGTGGAGGCCATCGGAAACCTGGAGATCTGAGGCT AGCCATTGAGGAAG <u>CTAGAACGATGAAGAAGAAGAAGATGATGA</u> TGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG	6785
	ATCGTTCT <u>CAAGAAGAA</u>	6786
	ATCGTTCT <u>CAAGAAGAA</u>	6787
	GAGGAAG <u>CTAGAACGAT</u>	6788
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Leu3Term TTG-TAG	AAAGTTAAAGCCGTCCAAAACCCAAACCAAGGAAAGGCAAACGAA AAGAAAAAA <u>ATGGCTT</u> <u>AGAATT</u> TAATGCCATCGCCTCGAAATCTCA GAAGCTCCCTGCTTGCTCTTCCACCAAA TTTGGTGGAAAGAGCAAAGCAAGGGAGCTTGAGATTGAGGCG ATGGCATTAAAT <u>CTAAGCCATT</u> TTTCGTTGCCTTCCT GGTTGGGTTTGACGGCTTTAACTT AATGGCTT <u>AGAATT</u> TA TAAAATT <u>CTAAGCCATT</u>	6789
	TTTGGTGGAAAGAGCAAAGCAAGGGAGCTTGAGATTGAGGCG ATGGCATTAAAT <u>CTAAGCCATT</u> TTTCGTTGCCTTCCT GGTTGGGTTTGACGGCTTTAACTT	6790
	AATGGCTT <u>AGAATT</u> TA	6791
	TAAAATT <u>CTAAGCCATT</u>	6792
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Ser1-Term TCG-TAG	CCCAAACCAAGGAAAGGCAAACGAAAAGAAAA <u>ATGGCTT</u> GAATT TAATGCCATCGCCT <u>AGAAT</u> CTCAGAACGCTCCCTGCTTGCTCTT CCACCAAAGGCCACCCCTAGATCTCCAA TTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAAAGCAAGG GAGCTCTGAGATT <u>CTAGGCGATGGCATT</u> AAATCAAAGCCATT TTTCTTCTGTTGCCTTCCTGGTTGGG CATCGCCT <u>AGAAT</u> CTC GAGATT <u>CTAGGCGATG</u>	6793
	TTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAAAGCAAGG GAGCTCTGAGATT <u>CTAGGCGATGGCATT</u> AAATCAAAGCCATT TTTCTTCTGTTGCCTTCCTGGTTGGG	6794
	CATCGCCT <u>AGAAT</u> CTC	6795
	GAGATT <u>CTAGGCGATG</u>	6796

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Lys11Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAATGGCTTGAATTTA ATGCCATCGCCTCG <u>T</u> AAATCTCAGAAGCTCCCTGCTTGCTCTCC ACCAAAGGCCACCCCTAGATCTCCCAAGT	6797
	ACTTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAAAGCAAG GGAGCTCTGAGATT <u>A</u> CGAGGCGATGGCATTAAAATTCAAAGCCA TTTTTCTTTCGTTGCCTTCCTGGTTG	6798
	TCGCCTCG <u>T</u> AAATCTCAG	6799
	CTGAGATT <u>A</u> CGAGGCGA	6800
Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Gln13Term CAG-TAG	AGGAAAGGCAAACGAAAAGAAAAATGGCTTGAATTTAATGCCA TCGCCTCGAAATCT <u>T</u> AGAAGCTCCCTGCTTGCTCTCCACCAAA GGCCACCCCTAGATCTCCCAAGTTTCCA	6801
	TGGAAAACCTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAA AGCAAGGGAGCTT <u>C</u> <u>A</u> AGATTTCGAGGCGATGGCATTAAAATTCAA AGCCATTTTCTTTCGTTGCCTTCCT	6802
	CGAAATCT <u>T</u> AGAAGCTC	6803
	GAGCTTCT <u>A</u> AGATTCG	6804

**Table 24**  
**Oligonucleotides to produce plants with reduced linolenic acid**

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTCTCTTTCTTGGGAAGAGGC TCCAATGGCGAGCT <u>AGGTTT</u> TATCAGAATGTGGTTAGACCTCTC CCCAGATTCTACCCCTAACACACAAACCTC	6805
	GAGGTTGTGTGTTAGGGTAGAATCTGGGGAGAGGTCTAAACCA CATTCTGATAAAAC <u>CTAGCTCGCCATTGGAGCCTCTCCCAAGAAG</u> AAAAGAGGAAAAAGTCTGTGTTCTATT	6806
	GGCGAGCT <u>GGTTT</u> TAT	6807
	ATAAAACCA <u>AGCTCGCC</u>	6808
	ACGACAGAGACTTTCTCTTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTT <u>GATCAGAATGTGGTTAGACCTCTCCCCAG</u> ATTCTACCCCTAACACACAAACCTCTTTGC	6809
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Leu6Term TTA-TGA	GCAAAAGAGGTTGTGTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGAT <u>CAAACCGAGCTCGCCATTGGAGCCTCTCC</u> CAAGAAGAAAAGAGGAAAAAGTCTGTGTCGTT	6810
	CTCGGTT <u>GATCAGAAT</u>	6811
	ATTCTGAT <u>CAAACCGAG</u>	6812
	ACAGAGACTTTCTCTTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTT <u>TATGAGAATGTGGTTAGACCTCTCCCCAGATT</u> C TACCCCTAACACACAAACCTCTTTGCCTC	6813
	GAGGCAAAAGAGGTTGTGTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCT <u>CATAAAACCGAGCTCGCCATTGGAGCCTCTT</u> CCCAAGAAGAAAAGAGGAAAAAGTCTCTGT	6814
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser7Term TCA-TGA	GGTTT <u>TATGAGAATGTG</u>	6815
	CACATTCT <u>CATAAAACC</u>	6816
	AGAGACTTTCTCTTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTT <u>TATCATAATGTGGTTAGACCTCTCCCCAGATT</u> CTA CCCTAACACACAAACCTCTTTGCCTCTA	6817
	TAGAGGCAAAAGAGGTTGTGTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATT <u>TATGATAAAACCGAGCTCGCCATTGGAGCCTC</u> TTCCAAGAAGAAAAGAGGAAAAAGTCTCT	6818
	TTTT <u>TATCATAATGTGGT</u>	6819
Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Glu8Term GAA-TAA	ACCACATT <u>TATGATAAAA</u>	6820

	Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu4Term TTG-TAG	TCATCATCTCTCTCTGGGGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAAGTGGTCTTATCCGAATGTGGCATAAGACCTCTCCCCAGATCCAC	6821
		GTGGATCTGGGTGTGGTAGATTCTGGGGAGAGGTCTTATGCCACATTGGATAAGACCTAGTTGCCATTGCTAGAGCTCTTTGCTCTCTCTCCCCAGAAGAAGATGATGA	6822
		GGCGAAGTGGTCTTATGGCAATGTGGCATAAGACCTCTCCCCAGATCCAC	6823
		ATAAGACCTAGTTGCC	6824
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu6Term TTA-TGA	TCTCTTCTCTGGGGAGAGAGAGAGCAAAAGAGCTCTAGCAAATGGCGAAGTGGTCTGATCCGAATGTGGCATAAGACCTCTCCCCAGATCCAC	6825
		GAATCTACACCACACCCAGATCCACTTCCCTAGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGGAGAGGTCTTATGCCACATTGCTAGAGCTCTTCTCTCTCCCCAGAAGAAGAAGA	6826
		ATGCCACATTGGATCAGACCAAGTTCGCCATTGCTAGAGCTCTTCTGGTCTGATCCGAAT	6827
		ATTGGATCAGACCAAG	6828
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Glu8Term GAA-TAA	TTCTCTGGGGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACATTGGTCTTATCCCTAATGTGGCATAAGACCTCTCCCCAGAATCTACACCACACCCAGATCCACTTCCCTCTCCA	6829
		TGGAGAGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGGAGAGGTCTTATGCCACATTAGGATAAGACCAAGTTCGCCATTGCTAGAGCTCTTGTCTCTCTCTCCCCAGAAGAA	6830
		TCTTATCCCTAATGTGGC	6831
		GCCACATTAGGATAAGA	6832
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Cys9Term TGT-TGA	CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAAGTGGTCTTATCCGAATGAGGCATAAGACCTCTCCCCAGAATCTACAC	6833
		CACACCCAGATCCACTTCCCTCTCCAACACCGGTGTTGGAGAGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGAGAGGTCTTATGCCCTAATCGGATAAGACCAAGTTCGCCATTGCTAGAGCTCTTGTCTCTCTCTCCCCAG	6834
		TCCGAATGAGGCATAAG	6835
		CTTATGCCCTCATTGGAA	6836
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Trp5Term TGG-TGA	ATAACAGAATTGCTGAATTCTGCATTTAGCTCTGGGTTCAA	6837
		TGGCTGCTGGTTGAGTATTATCAGAATGTGGTTAAGGCCTCTCCCCAGAATCTACTCACGACCCAGAATTGGT	6838
30		ACCAATTCTGGGTGAGTAGATTCTGGGAGAGGCCTAAACCACTTCTGATAATACCAACCAAGCAGCCATTGAAAACCCAGAAGCTTAAATGCAAGAATTCAAGAATTCTGTTAT	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTGGTT <u>GAGT</u> ATTATC	6839
	GATAATAC <u>TCA</u> ACCAGC	6840
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Leu7Term TTA-TGA	AGAATTGCTGAATTCTGCATTTAGCTTCTGGGTTTCATGGCT GCTGGTTGGGTAT <u>GAT</u> CAGAATGTGGTTAAGGCCTCTCCCAAGA ATCTACTCACGACCCAGAATTGGTTTAC	6841
	GTAAAACCAATTCTGGGCGTGAGTAGATTCTGGGAGAGGCCTT AAACCACATTCTGAT <u>CATA</u> ACCCAACCAGCAGCCATTGAAAACCCAG AAGCTAAAATGCAAGAATTCAATTCT	6842
	TTGGGTAT <u>GAT</u> CAGAAT	6843
	ATTCTGAT <u>CATA</u> ACCAA	6844
	ATTGCTGAATTCTGCATTTAGCTTCTGGGTTTCATGGCTGCT GGTTGGGTATTAT <u>GAGA</u> ATGTGGTTAAGGCCTCTCCCAAGAATCT ACTCACGACCCAGAATTGGTTTACATC	6845
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Ser8Term TCA-TGA	GATGTAAAACCAATTCTGGGCGTGAGTAGATTCTGGGAGAGGC CTTAAACCACATTCT <u>CATA</u> ACCCAACCAGCAGCCATTGAAAACC CAGAAGCTAAAATGCAAGAATTCAATTCT	6846
	GGTATTAT <u>GAGA</u> ATTGTG	6847
	CACATTCT <u>CATA</u> ATACC	6848
	TGCTGAATTCTGCATTTAGCTTCTGGGTTTCATGGCTGCT GTTGGGTATTAT <u>CATA</u> ATGTGGTTAAGGCCTCTCCCAAGAATCTA CTCACGACCCAGAATTGGTTTACATCGA	6849
	TCGATGTAAAACCAATTCTGGGCGTGAGTAGATTCTGGGAGAG GCCTTAAACCACATT <u>A</u> TGATAATACCCAACCAGCAGCCATTGAAAA CCCAGAACGCTAAAATGCAAGAATTCAATTCT	6850
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Glu9Term GAA-TAA	TATTAT <u>CATA</u> ATGTGGT	6851
	ACCACATT <u>A</u> TGATAATA	6852
	GCAAGTTGGGTTTATCAGAATGTGGCTTAGACCACTCCCAAGAA TCTACCCCTAAGCCCT <u>GAA</u> CTGGGCAGCCACTTCTGCCTCCTCTC ACATTAAGTTGAGAATTTCACGTACAGATC	6853
	GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGGAGGCAGAAGT GGCTGCCCTAGTC <u>A</u> GGGCTTAGGGTAGATTCTGGGAGTGGTCT AAGACCACATTCTGATAAAACCCAACTTGC	6854
	CTAAGCCCT <u>GAA</u> CTGGG	6855
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg22Term AGA-TGA	CCCAGTT <u>CAGGG</u> CTTAG	6856

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Lys34Term AAG-TAG	CTCCCAGAACCTACCCCTAACGCCAGAACCTGGGGCAGCCACTTCTGCCT GCCTCCTCTCACATTAGTTGAGAATTACGTACAGATCTGAGTG GTTCTGCAATTCTTGTCTAATACTAATA	6857
		TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG TGAAATTCTCAACTAAATGTGAGAGGAGGCAGAAGTGGCTGCC AGTTCTGGCTTAGGGTAGATTCTTGGGAG	6858
		CTCACATTAGTTGAGA	6859
		TCTCAACTAAATGTGAG	6860
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Leu35Term TTG-TAG	CAAGAACCTACCCCTAACGCCAGAACCTGGGGCAGCCACTTCTGCCT CCTCTCACATTAAGTAGAGAATTACGTACAGATCTGAGTG TGCAATTCTTGTCTAATACTAATAAAGA	6861
		TCTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT ACGTGAAATTCTCTACTTAATGTGAGAGGAGGCAGAAGTGGCTGC CCCAGTTCTGGCTTAGGGTAGATTCTT	6862
		CATTAAGTAGAGAATT	6863
		AAATTCTCTACTTAATG	6864
		AGAACCTACCCCTAACGCCAGAACCTGGGGCAGCCACTTCTGCCTCC TCTCACATTAAGTTGGAATTACGTACAGATCTGAGTG CAATTCTTGTCTAATACTAATAAAGAGA	6865
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg36Term AGA-TGA	TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT GTACGTGAAATTCAACCTTAATGTGAGAGGAGGCAGAAGTGGCT GCCAGTTCTGGCTTAGGGTAGATTCT	6866
		TTAAGTTGGAATTCA	6867
		TGAAATTCAACCTAA	6868
		GCGAGTTGGTTTATCAGAACATGTGGCTGAGGCCACTCCGAGG GTCTATCTAACGCCATGAACCTGGCCACCCCTTGTGAATTCCAATC CCACAAAGCTGAGATTTCAGAACAGATC	6869
		GATCTGTTCTGAAAATCTCAGCTTGTGGATTGGAATTCAACAA AGGGTGGCCAGTTCATGGCTTAGGATAGACCCTCGGGAGTGGCC TCAGACCACATTCTGATAAAACCCAACTCGC	6870
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Arg22Term AGA-TGA	CTAACGCCATGAACCTGGC	6871
		GCCAGTTCATGGCTTAG	6872
		CAGAACATGTGGCTGAGGCCACTCCGAGGGCTATCTAACGCCAA GAACATGGCCACCCCTAAGTTGAATTCCAATCCCACAAAGCTGAGATT TTCAAGAACAGATCTGGAAATGGTCTTC	6873
		GAAGAACACATTCCAAGATCTGTTCTGAAAATCTCAGCTTGTGG GATTGGAATTCAACTAAGGGTGGCCAGTTCTGGCTTAGGATAGA CCCTCGGGAGTGGCTCAGACCACATTCTG	6874
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG		
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CCACCCT <u>TAGTTGA</u> ATT	6875
	AATTCAACT <u>AAGGGT</u> GG	6876
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu28Term TTG-TAG	AATGTGGTCTGAGGCCACTCCGAGGGTCTATCCTAAGCCAAGAA CTGGCCACCC <u>TTGT</u> <u>AGA</u> ATTCCAATCCCACAAAGCTGAGATTTCA AAGAACAGATCTTGGAAATGGTTCTTCATT	6877
	AATGAAGAACCA <u>TTCCA</u> AGATCTGTTCTGAAAATCTCAGCTTGT GGGATTGGAA <u>TTCT</u> ACAAAGGGTGGCCAGTTCTGGCTTAGGATA GACCCTCGGGAGTGGCCTCAGACCACATT	6878
	CCCTTG <u>TAGA</u> ATTCCA	6879
	TGGAATT <u>CTACAAAGGG</u>	6880
	CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCC <u>TTGTTG</u> AATTCCAATCCCACATAGCTGAGATTTCAAGAACAGATCTTGGAA ATGGTTCTTCATTCTGTTGTCAGTGGGA	6881
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Lys34Term AAG-TAG	TCCC <u>ACTCGACA</u> AAACAGAACGAA <u>ATGAGAACCA</u> TTCCAAGATCTGTTCT TGAAAATCTCAG <u>CTATGT</u> GGGATTGGAA <u>ATTCAACAAAGGGTGGCC</u> AGTTCTTGGCTTAGGATAGACCCTCGGGAG	6882
	ATCCCAC <u>ATAGCTGAGA</u>	6883
	TCTCAG <u>CTATGT</u> GGGAT	6884
	CATCAGAGCGGC <u>GATA</u> CCCTAAC <u>CTAACG</u> ATTGCTGGGTAAGAACATCCATG GAAGT <u>CTATGAGT</u> TA <u>GGT</u> CGTCAGAGAGCTAGCCATCGTGGT <u>CGC</u> ACTAGCTGCTGGAG <u>CTGCT</u> AC <u>CTCAACAA</u> AT	6885
	ATTGTTGAGGTAAGCAG <u>CTCCAGCAGCAG</u> CTAGTG <u>CGAACACGATGGC</u> TAGCTCTGAC <u>GACCTA</u> ACTCATAGACTCCATGGATT <u>CTTAACC</u> CAGCAAT <u>GCTTAGGT</u> ATGCCGCT <u>CTGATG</u>	6886
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Tyr3Term TAC-TAG	ATGAG <u>TTAGGT</u> CGTCAG	6887
	CTGACGAC <u>CTAACTCAT</u>	6888
	GC <u>GGCGATA</u> CCCTAAC <u>CTAACG</u> ATTGCTGGGTAAGAACATGGAA <u>GTCT</u> ATGAGTTAC <u>GTGTC</u> <u>T</u> <u>GAGAGCTAGCCATCGTGGT</u> CGCA <u>CTAGCT</u> GCTGGAG <u>CTGCT</u> AC <u>CTCAACAA</u> TTGG <u>CTTG</u>	6889
	CAAG <u>CCAATTGTTGAGGTAAGCAGCAG</u> CTCCAGCAG <u>CTAGTGCGAAC</u> CGATGG <u>CTAGCTCTC</u> <u>A</u> <u>GACGACGTA</u> ACTCATAGACTCCATGGAT TCTTAACCCAG <u>CAATGCTTAGGT</u> ATGCCG <u>CG</u>	6890
	ACGTC <u>GTCT</u> <u>TGAGAGCTA</u>	6891
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Arg6Term AGA-TGA	TAGCT <u>CTCA</u> <u>GACGACGT</u>	6892

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Glu7Term GAG-TAG	GCGATACCTAACGATTGCTGGGTTAAGAACATGGAAAGTCTATGA GTTACGTCGTCAAGATAGCTAGCCATCGTGTGCACTAGCTGCTG GAGCTGCTTACCTAACAAATTGGCTTGT AAACAAGCCAATTGGTAGGTAAGCAGCTCCAGCAGCTAGTGCGA ACACGATGGCTAGCTATCTGACGACGTAACTCATAGACTTCATG GATTCTAACCCAGCAATGCTTAGGTATCGC	6893
		TCGTCAGATAGCTAGCC	6895
		GGCTAGCTATCTGACGA	6896
		CCATGGAAAGTCTATGAGTTACGTCGTCAAGAGAGCTAGCCATCGT TTCGCACTAGCTGCTTGAGCTGCTTACCTAACAAATTGGCTTGT GGCCTCTTATTGGATTGCTCAAGGAACCA	6897
		TGGTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTT GAGGTAAGCAGCTCAAGCAGCTAGTGCACACGATGGCTAGCT CTCTGACGACGTAACTCATAGACTTCATGG	6898
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Gly17Term GGA-TGA	TAGCTGCTTGAGCTGCT	6899
		AGCAGCTCAAGCAGCTA	6900
		GCAAGTGGGTTCTATCAGAACATGGCTTAGACCACCAAGAA TATACCCAAAGCCCTGAATAGGGTCTTCCGTTGCCACCAA TTAAATCTGAGAAGAATTTCACCTTCAC	6901
		GTGAAGGTGAAATTCTCTCAGATTAAATTGGTGGCGCAAACGGA AGAAGACCCATTCAAGGGCTTGGGTATATTCTGGTAGTGGCTA AGACCACATTCTGATAGAACCCAACTTGC	6902
		CAAAGCCCTGAATAGGG	6903
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg22Term AGA-TGA	CCCTATTCAAGGGCTTTG	6904
		TGGCTTAGACCAACTACCAAGAACATACCCAAAGCCCAGAACATGG GTCTTCTCCGTTGAGCCACCAATTAAATCTGAGAACGAAATTCA CCTTCACCTATACGAACAGATCGAACATTGT	6905
		ACAATTCCGATCTGTCGTAGGTGAAGGTGAAATTCTCTCAGA TTAAATTGGTGGCTCAAACGGAGAACGACCTATTCTGGCTTTG GGTATATTCTGGTAGTGGCTAACACCA	6906
		TCCGTTGAGCCACCAA	6907
		TTGGTGGCTCAAACGGGA	6908
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Cys29Term TGC-TGA	CACTACCAAGAACATACCCAAAGCCCAGAACATAGGGTCTTCCGT TTGCGCCACCAATTGAAATCTGAGAACGAAATTCAACCTCACCTATA CGAACAGATCGAACATTGTTGGCATTGAG	6909
		CTCAATGCCAACAAATTCCGATCTGTCGTAGGTGAAGGTGAAA TTCTTCTCAGATTCAATTGGTGGCGAACCGGAAGAACGACCTAT TCTGGCTTGGGTATATTCTGGTAGTG	6910
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Leu33Term TTA-TGA		
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CACCAATT <u>GAAATCTGA</u>	6911
	TCAGATT <u>CAATTGGTG</u>	6912
Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg36Term AGA-TGA	AGAATATA <u>CCCAAAGCCCAGAATAGGGTCTTCCGTTGCGCCA</u> CCAATT <u>AAATCTGTGAAGAATTTCACCTCACCTATACGAACAGAT</u> CGGAATT <u>GGTGGGCATTGAGGGTAAGTG</u> CACTTACCC <u>CTCAATGCCAACAAATTCCGATCTGTCGTATAGGTGA</u> AGGTGAA <u>ATTCTTCACAGATTAAATTGGTGGCGAACACGGAAGAA</u> GACCCTATT <u>CTGGGCTTGGGTATATTCT</u> TAAAT <u>CTGTGAAGAATT</u>	6913 6914 6915 6916
Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Trp4Term TGG-TGA	CTCTTTATT <u>ATCCCTCTTCTTGT</u> TTT <u>GAGTTCTGAGTCACC</u> TATGGCAAG <u>TTGAGTGATTTCAGAATGTGGCTAAGGCCACTTCC</u> AAGAAT <u>CTATGCCAGGCCAGAAGTGG</u> TCCACTT <u>GGGCCTGGCATAGATTCTGGAAGTGGCCTAGCCC</u> ACATT <u>CTGAAATCACCAACTGCCATAGGTGACTCAGAACTCAA</u> AAAA <u>ACAAGAAGAGGAGGATAATAAGAG</u> GCAAG <u>TTGAGTGATTTC</u> GAAAT <u>CACCAACTTGC</u>	6917 6918 6919 6920
Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Ser7Term TCA-TGA	TATCCTCC <u>CTTCTTGT</u> TTT <u>GAGTTCTGAGTCACCTATGGCA</u> AGTTGGGT <u>GATTTGAGAATGTGGCTAAGGCCACTTCCAAGAAC</u> TATGCC <u>AGGCCAGAAGTGGAGCTTCATG</u> CATGAAG <u>CTCCACTTCTGGCCTGGCATAGATTCTGGAAGTGGC</u> CTTAG <u>CCCACATTCTCAAATCACCAACTGCCATAGGTGACTCAG</u> AACT <u>CAAAAAAAACAAGAAGAGGAGGATA</u> GGT <u>GATTGAGAATGTG</u> CACATT <u>CTCAAATCAC</u>	6921 6922 6923 6924
Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Glu8Term GAA-TAA	TCCTCCT <u>CTTCTTGT</u> TTT <u>GAGTTCTGAGTCACCTATGGCAAG</u> TTGGGT <u>GATTCAAAATGTGGCTAAGGCCACTTCCAAGAAC</u> GCC <u>AGGCCAGAAGTGGAGCTTCATGTT</u> AACAT <u>GAAGCTCCACTTCTGGCCTGGCATAGATTCTGGAAGTG</u> GCCT <u>TAGCCCACATTATGAAATCACCAACTGCCATAGGTGACTC</u> AGAA <u>CTCAAAAAAAACAAGAAGAGGAGGATA</u> TGATT <u>TCATAATGTGGG</u> CCCACATT <u>TGAAATCA</u>	6925 6926 6927 6928

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Cys9Term TGT-TGA	CTCTTCTTGT <del>TTT</del> TGAGTTCTGAGTCACCTATGGCAAGTTGGG TGAT <del>TT</del> CAGAATGAGGGCTAAGGCCACTTCCAAGAATCTATGCCA GGCCCAGAAGTGGAGCTTCATGTTCAAC	6929
		GTTGAAACATGAAGCTCCACTTCTGGGCTGGCATAGATTCTTGGA AGTGGCCTAG <del>CCC</del> CTCATTCTGAAATCACCCAAC <del>T</del> TGCCATAGGTG ACTCAGAACTCAAAAAAAACAAAGAAGAG	6930
		TCAGAATG <del>A</del> GGGCTAAG	6931
		CTTAG <del>CCC</del> CTCATTCTGA	6932
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Lys21Term AAA-TAA	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTA ATGG <del>TTT</del> CATGCT <del>T</del> AAGAAGAAGAAGAAGAGGATTTCGACTT AAGCAATCCTCCTCCATTCAATATTGGTC	6933
		GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTC TTCTTCTTCTTCTT <del>A</del> AGCATGAAAACCATTAACGCCATTAGAATTG GGGTGTCTTGTACTGTTGCTGCTTCAT	6934
		TTCATGCT <del>T</del> AAGAAGAA	6935
		TTCTTCTT <del>A</del> AGCATGAA	6936
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu22Term GAA-TAA	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATG GTTT <del>T</del> CATGCT <del>A</del> ATAAGAAGAAGAAGAAGAGGATTTCGACTTAAG CAATCCTCCTCCATTCAATATTGGTCAGA	6937
		TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC TTCTTCTTCTTCTT <del>A</del> TTAGCATGAAAACCATTAACGCCATTAGAA TTGGGTGTCTTGTACTGTTGCTGCTT	6938
		ATGCTAA <del>A</del> AGAAGAA	6939
		TTCTTCTT <del>A</del> TTAGCAT	6940
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu23Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCT <del>A</del> AGA <del>A</del> TAAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6941
		GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTT <del>A</del> TTCTT <del>A</del> AGCATGAAAACCATTAACGCCATTAA GAATTGGGGTGTCTTGTACTGTTGCTG	6942
		CTAAAGA <del>A</del> TAAGAAGAA	6943
		TTCTTCTT <del>A</del> TTCTT <del>A</del> AG	6944
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu24Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCT <del>A</del> AGA <del>A</del> TAAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6945
		GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTT <del>A</del> TTCTT <del>A</del> AGCATGAAAACCATTAACGCCATTAA GAATTGGGGTGTCTTGTACTGTTGCTG	6946
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTAAAGAATAAGAAGAA	6947
	TTCTTCTT <u>ATT</u> CTTTAG	6948
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAAACATGTTGGTAATGGTGCAGGGAA AGAAGATCAAGCT <u>TA</u> GGTGTGATCCAAAGTGCTCCACCACCCCTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAA	6949
	TTTGGATTGCTGCTCTGATATTGCAATCTTGAAGGGTGGTGG GCACTGGATCAA <u>ACT</u> AAAGCTTGATCTCTTCCCTGCACCATTAC CAACATGTTGTAGAGGCTGTGCTGGACC	6950
	CAAGCT <u>TA</u> GGTGTGATCC	6951
	GGATCAA <u>ACT</u> AAAGCTTG	6952
	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTGATCCAAAGTG CTCCACCACCCCT <u>TA</u> GATTGCAAATATCAGAGCAGCAATTCCAAA ACATTGCTGGGAGAAGAACACATTGAGAT	6953
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Lys31Term AAG-TAG	ATCTCAATGTGTTCTCTCCAGCAATGTTGGATTGCTGCT GATATTGCAATCT <u>AGA</u> AGGGTGGTGGAGCAGTGGATCAAATAA GCTTGATCTCTTCCCTGCACCATTAC	6954
	CACCC <u>TTCT</u> <u>AG</u> ATTGCA	6955
	TGCAATCT <u>AGA</u> AGGGTG	6956
	AAAGAAGATCAAGCTTATTGATCCAA <u>GT</u> GCTCCACCACCCCTCA AGATTGCAAATATCT <u>G</u> AGCAGCAATTCCAAAACATTGCTGGGAGAA GAACACATTGAGATCTCTGAGTTATGTT	6957
	GAACATAACTCAGAGATCTCAATGTTCTCCAGCAATGTT GGAATTGCTGCT <u>CA</u> GATATTGCAATCTTGAAGGGTGGTGGAGCA CTTGGATCAAATAAGCTGATCTCTT	6958
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Arg36Term AGA-TGA	CAAATAT <u>CT</u> GAGCAGCA	6959
	TGCTGCT <u>CA</u> GATATTG	6960
	TATTTGATCCAA <u>GT</u> GCTCCACCACCC <u>CT</u> CAAGATTGCAAATATCA GAGCAGCAATT <u>CC</u> <u>TA</u> ACATTGCTGGGAGAAGAACACATTGAGATC TCTGAGTTATGTT <u>CT</u> GAGGGATGTGTTGG	6961
	CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTTCTT CTCC <u>CA</u> GCAATGTT <u>AT</u> GGATTGCTGCTGATATTGCAATCTG AAGGGTGGAGCAGTGGATCAAATA	6962
	CAATT <u>CC</u> <u>TA</u> ACATTGC	6963
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Leu41Term AAA-TAA	GCAATGTT <u>AT</u> GGATTG	6964

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Glu8Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCGCTGACGGCGGCAATGGC CCGGCTCGTGCTCTCCTAGTGCTCGGGCCTCGCGCCCGTCCGCC GCCTGCGCCGCCGGCCGGCGCCATTGCGGCCGC	6965
	GCGCCGCAATGGCGCCCCGGCCGGCGCAGGCGGGACGG GCGCGAGGCCCGAGCACTAGGAGAGCACGAGCCGGGCCATTGC CGCCGTAGCGGGCGGGTGCGGGTGCGGGTGGATG	6966
	TGCTCTCCTAGTGCTCG	6967
	CGAGCACTAGGAGAGCA	6968
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Cys9Term TGC-TGA	ACCCGCACCCGCACCCGCCCGCTGACGGCGGCAATGGCCCG CTCGTGCTCTCCGAGTGATCGGGCCTCGCGCCCGTCCGCCGC GCGCGCCGCCGGCGCCATTGCGGCCGC	6969
	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCAGGCGGG ACGGGCGCGAGGCCGATCACTCGGAGAGCACGAGCCGGCCA TTGCCGCGTCAGCGGGCGGGTGCGGGTGCGGGT	6970
	TCCGAGTGATCGGGCCT	6971
	AGGCCCGA <del>T</del> CACTCGGA	6972
	CCGCACCCGCACCCGCCCGCTGACGGCGGCAATGGCCCG CGTGCTCTCGAGTGCTAGGGCCTCGCGCCCGTCCGCCGC GCGCCGCCGGCGCCATTGCGGCCGC	6973
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser10Term TCG-TAG	GGTGACCCGCCGCAATGGCGCCCCGGCCGGCGCAGGCG GGACGGGCGCGAGGCCCTAGCACTCGGAGAGCACGAGCCGGC CATTGCCGCCGTAGCGGGCGGGTGCGGGTGC	6974
	CGAGTGCTAGGGCCTCG	6975
	CGAGGCCCTAGCACTCG	6976
	GCTCGGGCCTCGCGCCCGTCCGCCCTGCGCGCCGGCGGG CGCCATTGCGCGCGGTGACCCCCCGCGCTCTCGCGCG CGCCGTGTCCTCGCGTCCCGTCCACCGCGA	6977
	TCGCGGTGGATGGACGCGGACGCGGGACGACGGCGCG CGGAGAGCGCGGGGGTCAACCGCGCCGCAATGGCGCCCCGG GGCGCGCAGGCGGGACGGCGCGAGGCCCGAGC	6978
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser29Term TCA-TGA	GGCGCGGTGACCCCCCG	6979
	CGGGGGGTCAACCGCGCC	6980
	CCCCCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGC CCCCGCAATGAGGCCGTAGCAGGAGGCGAGCTGCAAGGCCACC GAGGACCAACCGCTCCGAGTTGACGCCGCCAAGC	6981
	GCTTGGCGCGTGAACCTGGAGCGGTGGTCTCGGTGGCCTTG CAGCTCGCCTCTGCTACGGCCTCATTGCGGGGGCATGGCCGC GGATGGATCTGTGCGTGTGCGTGGGGAGGGGG	6982
25 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu8Term GAG-TAG		
30 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu8Term GAG-TAG		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGAGGCCGTAGCAGGAG	6983
	CTCCTGCTACGGCCTCA	6984
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Gln9Term CAG-TAG	CCTCCCCACGCACACGCACAGATCCATCCGCCATGGCCCC CGCAATGAGGCCGGAGTAGGAGGCCAGCTGCAAGGCCACCGAG GACCACCGCTCCGAGTTGACGCCAGGCCAAGCCGC GCGGCTTGGCGCGCTCGAAGCTCGGAGCGGTGGTCTCGGTGGC CTTGAGCTCGCCCTACTCCGGCTCATTGCGGGGGCATGG CCGCGGATGGATCTGCGTGTGCGTGGGGAGG GGCCGGAGTAGGAGGCG	6985 6986 6987 6988
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu10Term GAG-TAG	CCCCCACGCACACGCACAGATCCATCCGCCATGGCCCCCGC AATGAGGCCGGAGCAGTAGGCGAGCTGCAAGGCCACCGAGGACC ACCGCTCCGAGTCGACGCCAGGCCAAGCCGC GCGCGGCTTGGCGCGCTCGAAGCTCGGAGCGGTGGTCTCGGT GGCCTTGCAGCTCGCTACTGCTCCGGCTCATTGCGGGGGCCA TGGCCGCGGATGGATCTGCGTGTGCGTGGGG CGGAGCAGTAGGCGAGC	6989 6990 6991 6992
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Cys13Term TGC-TGA	ACGCACAGATCCATCCGCCATGGCCCCCGCAATGAGGCCGG AGCAGGAGGCGAGCTGAAAGGCCACCGAGGACCACCGCTCCGA GTTGACGCCAGGCCAAGCCGCCCTCCGCATC GATGCGGAAGGGCGCGCTTGGCGCGCTCGAAGCTCGGAGCGG TGGTCCTCGGTGGCCTTTCAGCTCGCTCCTGCTCCGGCTCATT GCGGGGCCATGGCCGGATGGATCTGCGT GCGAGCTGAAAGGCCAC	6993 6994 6995 6996
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Ser4Term TCG-TAG	CTTCACAAATCACAAATCGGAATCAGATCCACCAAGACACCCCGG CGGCAATGGCGCGTAGGGGACCCAGGAGGCCACTGCAAGGC TTCCGAGGACGCCGTCTTCTCGACGCC GCGGCCTCGAAGAAGAGACGGGCGCTCGGAAGCCTGCAGTC GGCCTCTGGTCGCCTACGCCGCCATTGCCGCCGGGTGCGT GGTGGATCTGATTCGATTGTGATTGTGAAG GGCGCGTAGGCCACCC GGTCGCCCTACGCCGCC	6997 6998 6999 7000

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCAACGACACCCCGGCGGCAATG GCGGCGTCGGCGACCT <u>AGGAGGCC</u> ACTGCAAGGCTTCGAGG ACGCCCCTCTTCTCGACGCCGCCAAGCCCC	7001
	GGGGCTTGGCGGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAGTCGGCCTCCT <u>AGGT</u> CGCCACGCCGCCATTGCCGCCG	7002
	GGGTGTCGTGGTGGATCTGATTCCGATTGTGAT	
	CGGCGAC <u>CTAGGAGGCC</u>	7003
	GGCCTCCT <u>AGGT</u> CGCCG	7004
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCAACGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAGT <u>AGGCC</u> ACTGCAAGGCTTCGAGGACG CCCCTCTTCTCGACGCCGCCAAGCCCCCGC	7005
	GCGGGGGCTTGGCGGGCGTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGAGTCGGCCT <u>ACT</u> GGGTGCGCCACGCCGCCATTGCCG	7006
	CCGGGGTGTCTGGTGGATCTGATTCCGATTGT	
	CGACCCAG <u>TAGGCCGAC</u>	7007
	GTCGGCCT <u>ACT</u> GGGTGCG	7008
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Cys10Term TGC-TGA	TCAGATCCACCAACGACACCCCGGCGGCAATGGCGGCGTCGGCGA CCCAGGAGGCCGACTG <u>AAAGG</u> CTTCGAGGACGCCGTCTCTC TTCGACGCCGCCAAGCCCCGCCCTCCGCATC	7009
	GATGCGGAAGGGCGGGGCTTGGCGGCCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTT <u>TCAGT</u> CGGCCCTGGGTGCCGACGC	7010
	CGCCATTGCCGCCGGGTGCGTGGTGGATCTGA	
	GCCGACT <u>GAAAGGCTTC</u>	7011
	GAAGCCTT <u>TCAGTCGGC</u>	7012

## WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications of the oligonucleotide, said chemical modifications selected from the group consisting of an o-methyl modification, an LNA modification including LNA derivatives and analogs, two or more phosphorothioate linkages on a terminus, and a combination of any two or more of these modifications.
2. The oligonucleotide according to claim one that comprises two or more phosphorothioate linkages on at least the 3' terminus.
3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.
4. The oligonucleotide according to claim one that comprises an LNA nucleotide, including an LNA derivative or analog.
5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.
6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.
7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 4341-7012 .
8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in callus, comprising administering to the callus an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A plant organism comprising the cell according to claim 14.

16. A plant or plant part produced by the method of claim 11.

17. A method of determining whether an oligonucleotide is optimized for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a second oligonucleotide, said second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2'-O-methylated oligonucleotide and a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

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18. The method of claim 17 in which the alteration is produced in a plant cell extract.
19. The method of claim 17 in which the alteration is produced in a cell.
20. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2-O-methylated oligonucleotide and a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

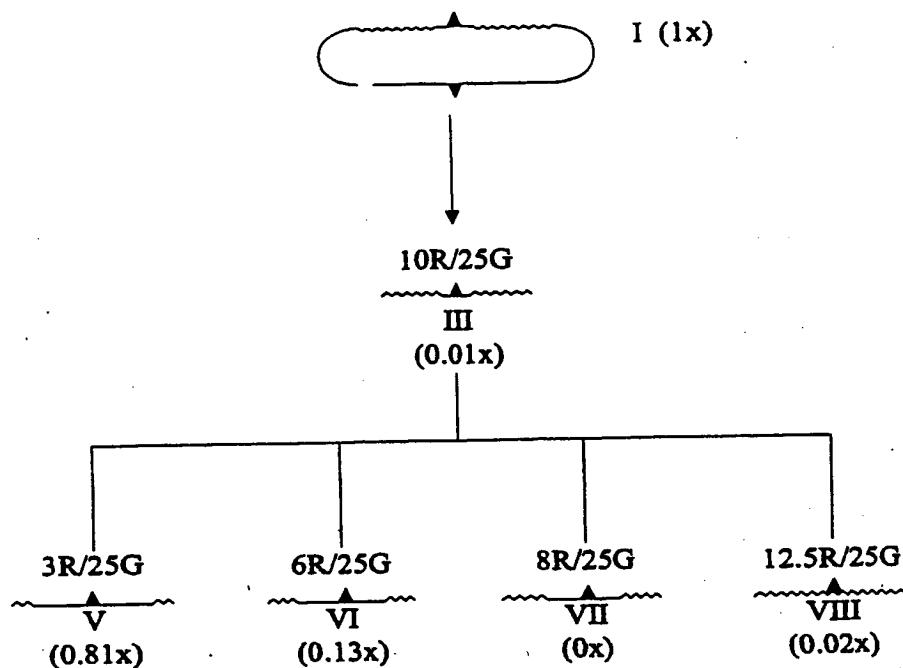


Figure 1A

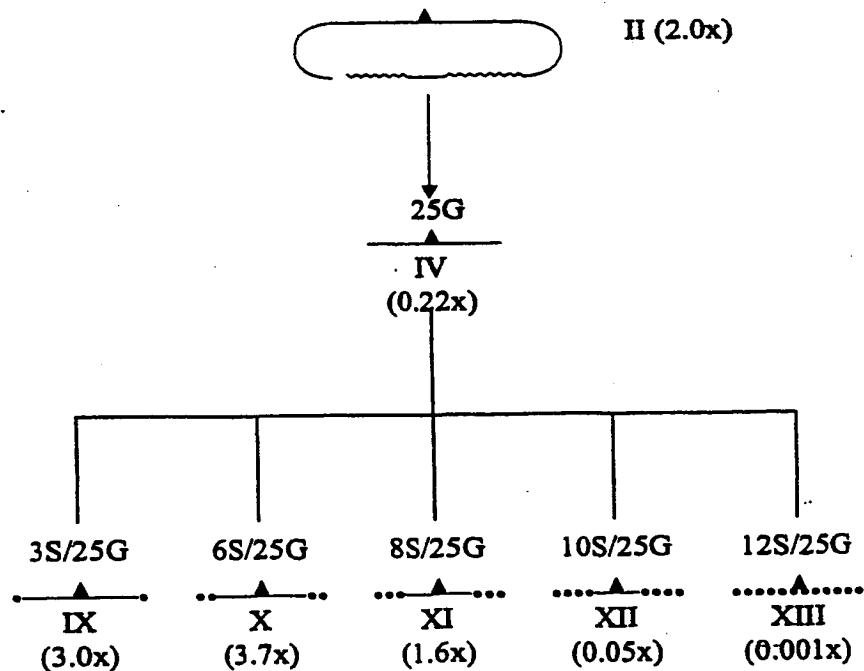


Figure 1B

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## Plasmids, DNA targets and chimeric oligonucleotides

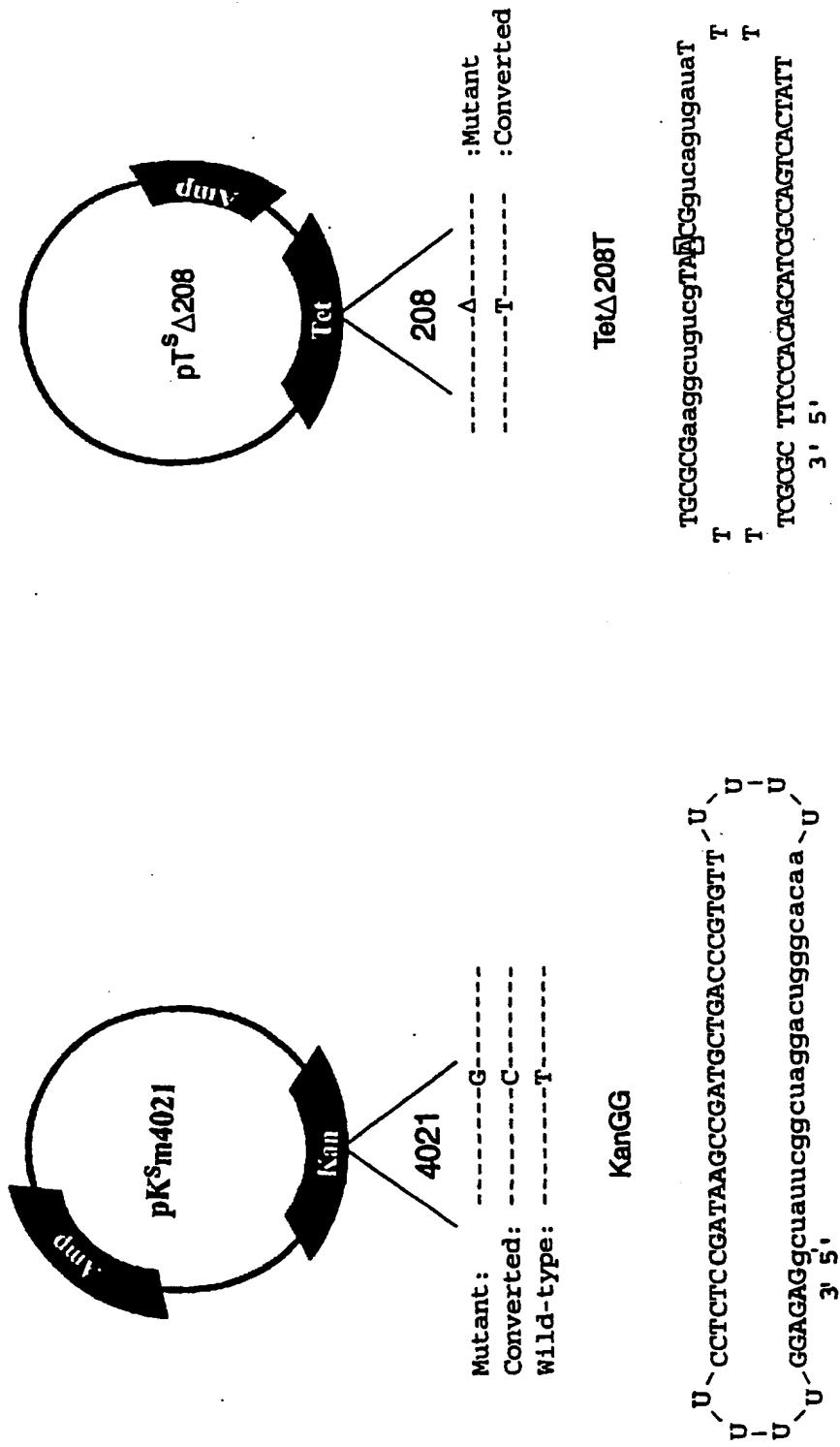


Figure 1C

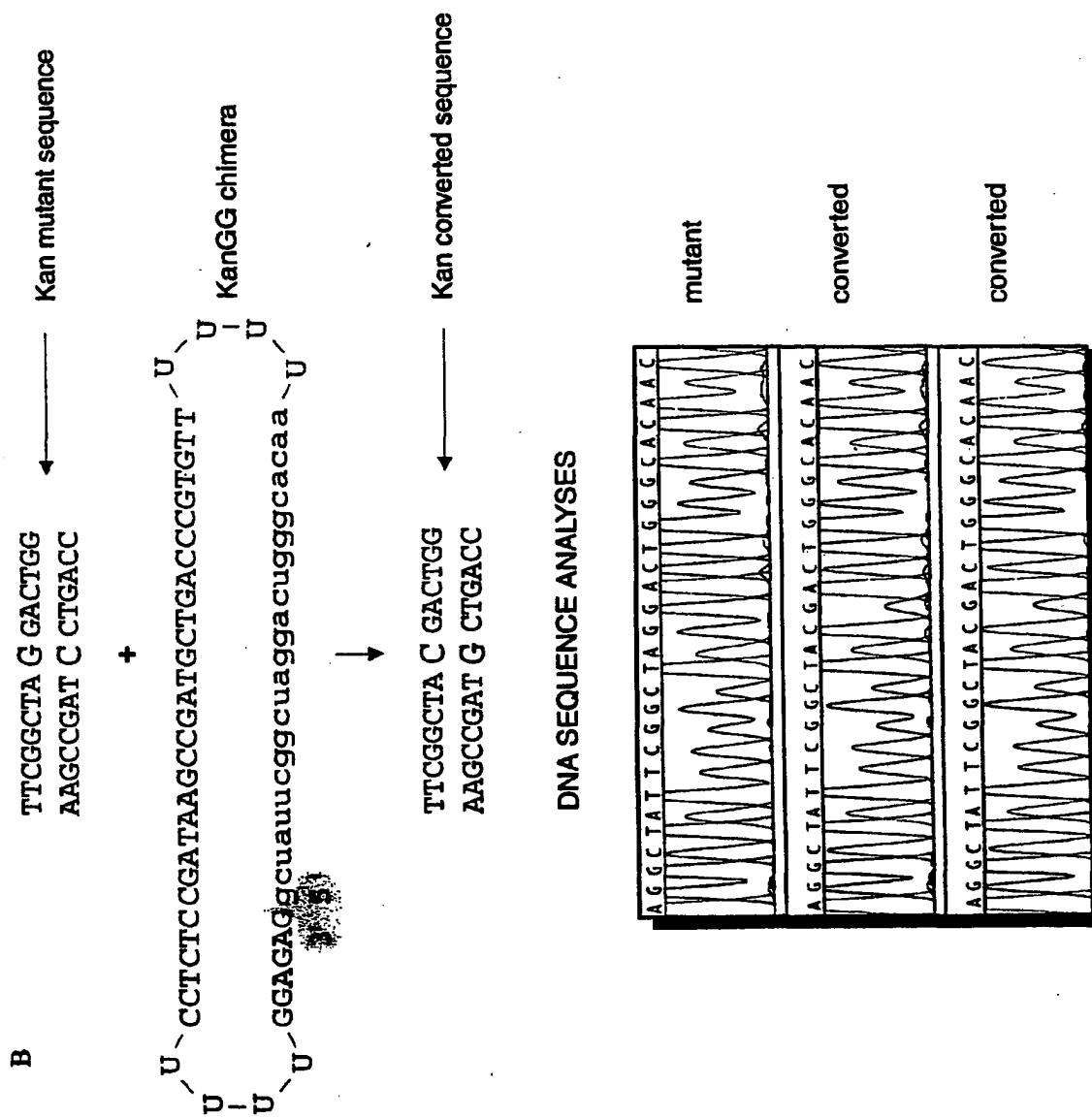


Figure 1D

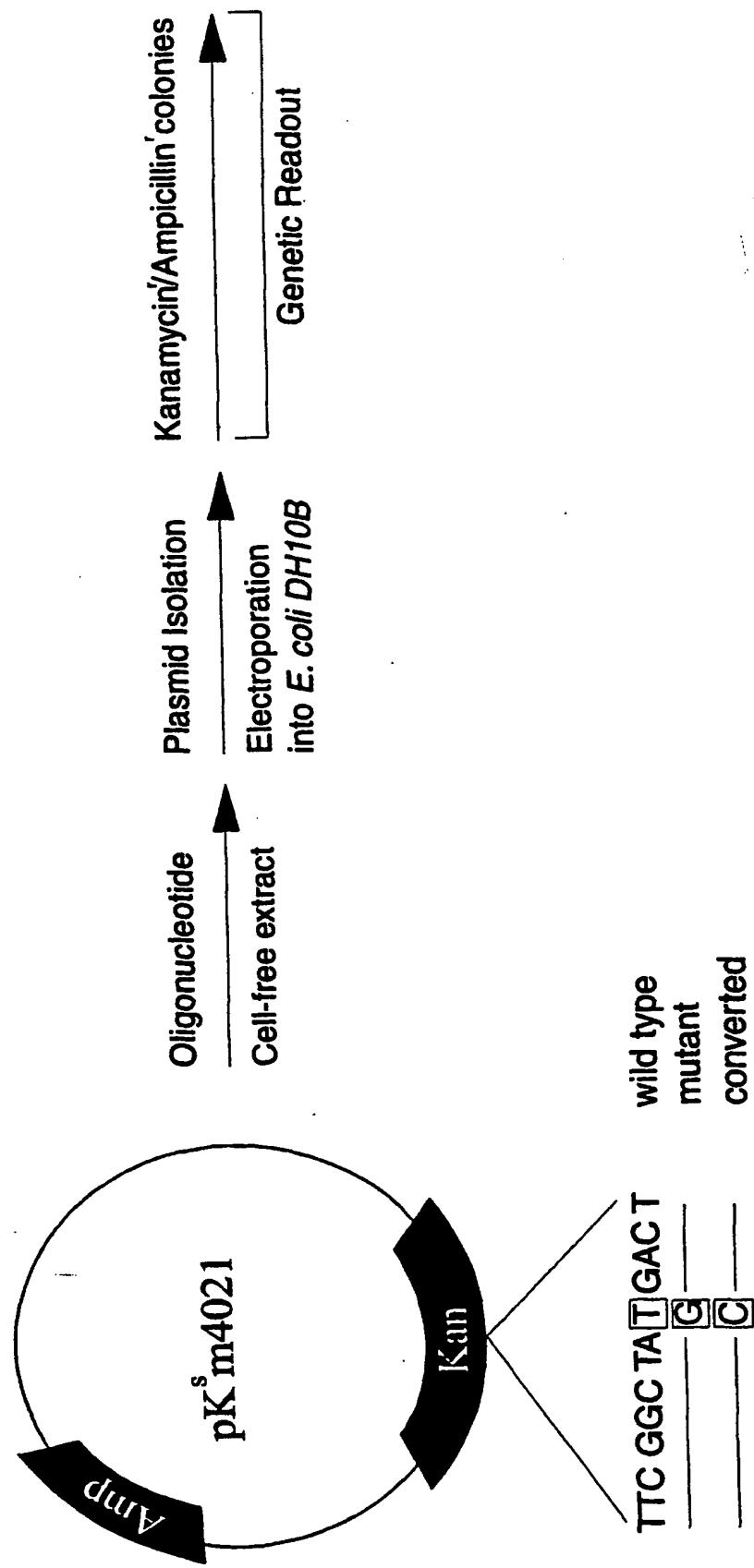


Figure 2

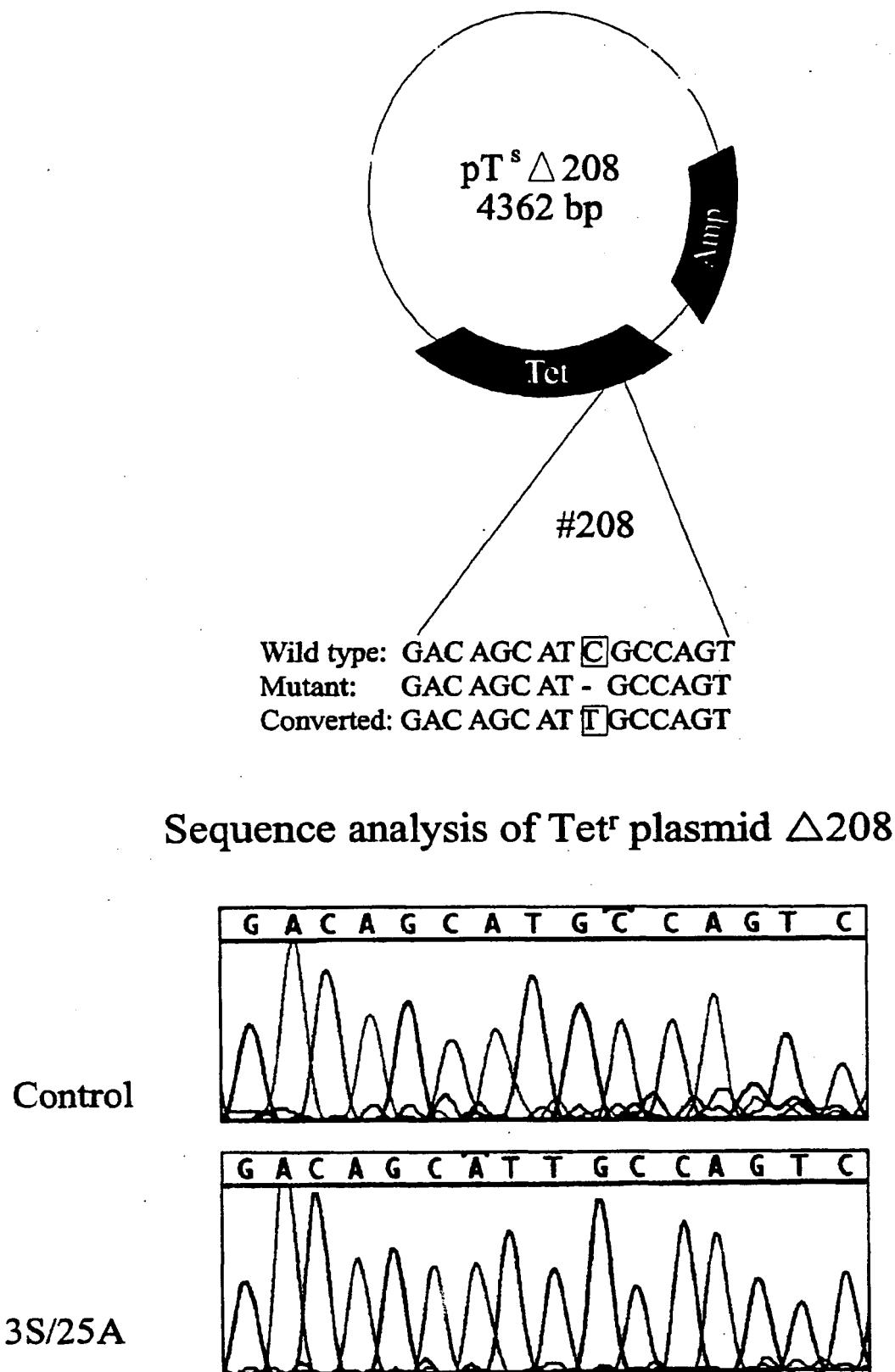


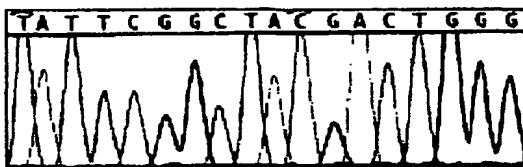
Figure 3

## DNA sequence analysis of Kan<sup>r</sup> plasmids

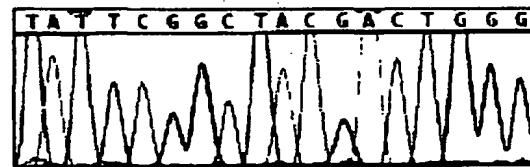
### Target codon distribution

oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	---	+	---	---	---
2) 6S/25G (20)	---	+	---	---	---
3) 8S/25G (20)	---	+	---	---	---
4) 10S/25G (18)	---	+	---	+(2)	+(2)
5) 25S/25G (4)	---	---	+(2)	+(2)	---

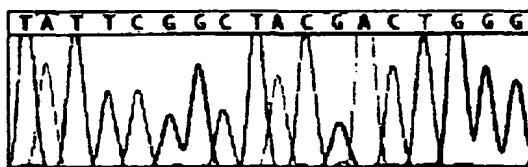
3S/25G



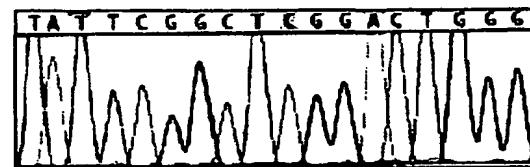
6S/25G



8S/25G



10S/25G



25S/25G



25S/25G

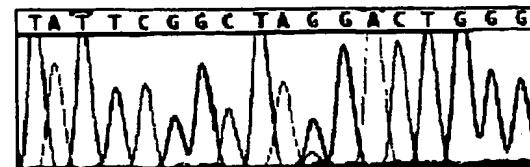
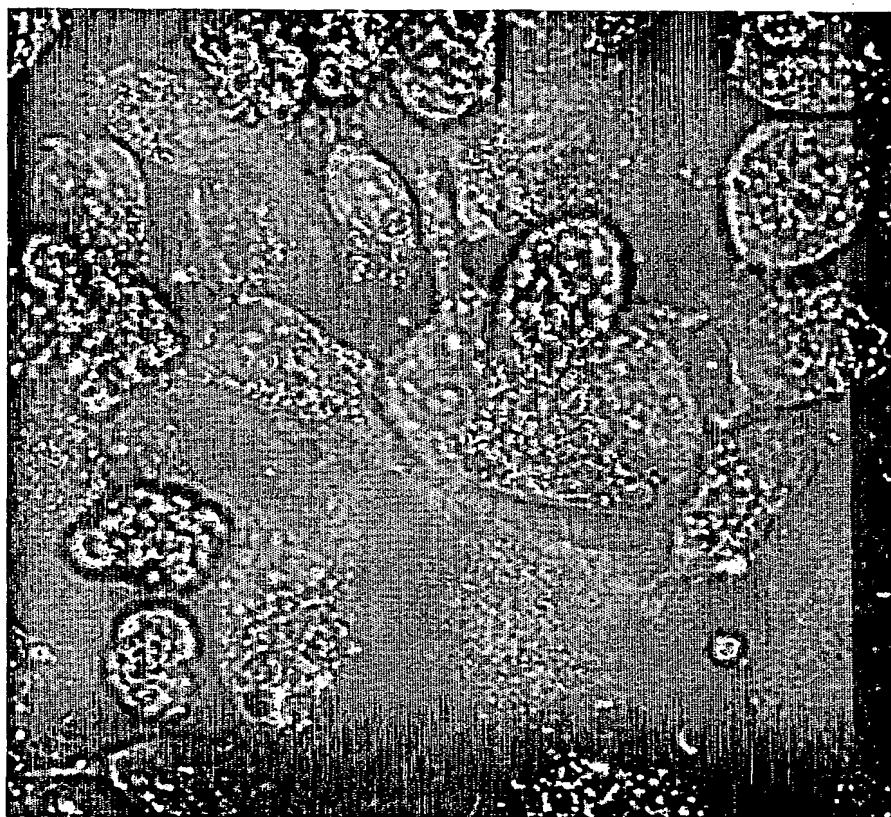


Figure 4



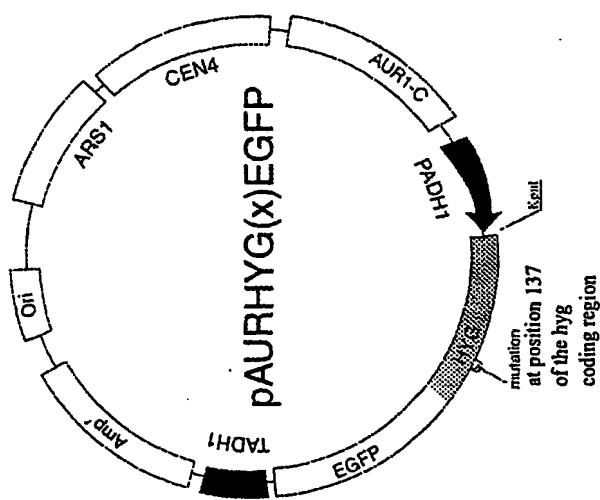
**Figure 5**



**Figure 6**

Sequence of normal allele: GTGGATAATGTCCCT  
 Target/existing mutant: GTGGATAATGTCCCT  
 Desired alteration: GTGGATAACGTCCCT

Figure 7A



Sequence of normal allele: GTGGATAATGTCCCT  
 Target/existing mutant: GTGGATAAGTCCCT  
 Desired alteration: GTGGATAACGTCCCT

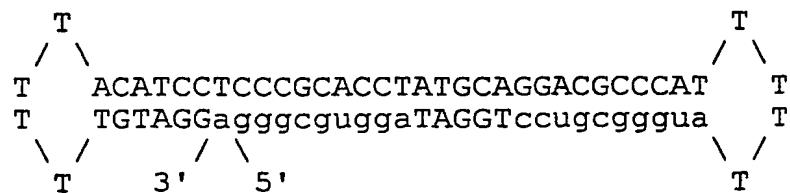
Figure 7B

HyqE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HyqE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC  
GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG  
CCG ATG GTT TCT AC-3'

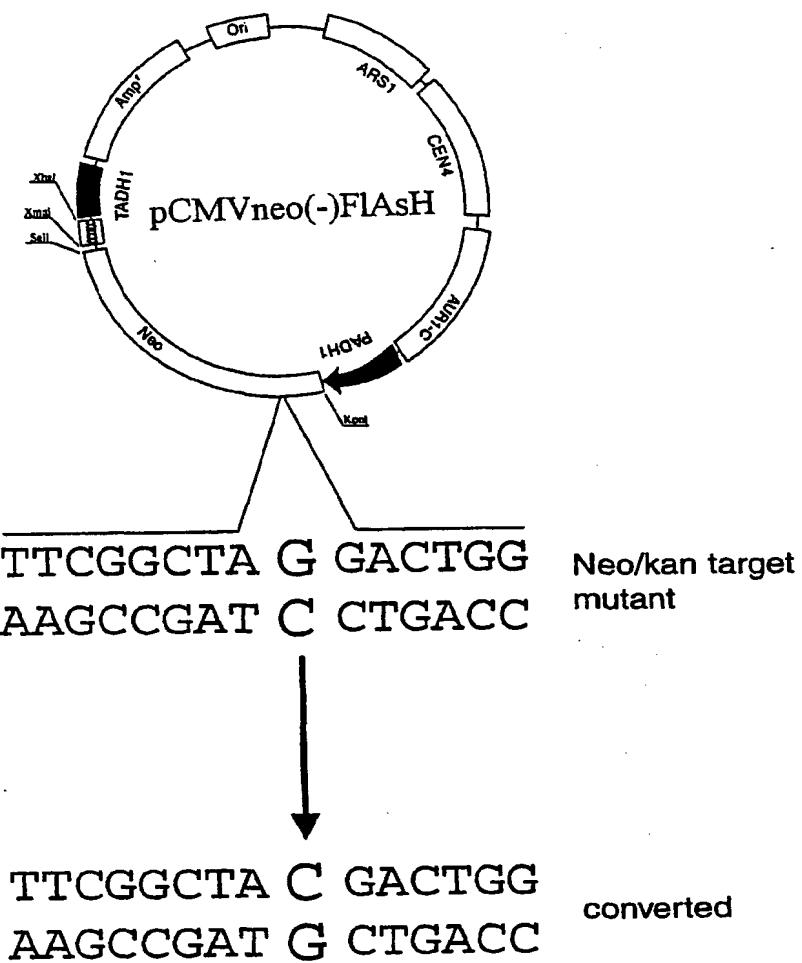
HyqE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG  
CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA  
GCT GAA AGC ACG AG-3'

HyqGG/Rev:



Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTG CCC AGT  
CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG  
A-3'

Figure 8



### FUSION GENE FOR LIGAND BINDING

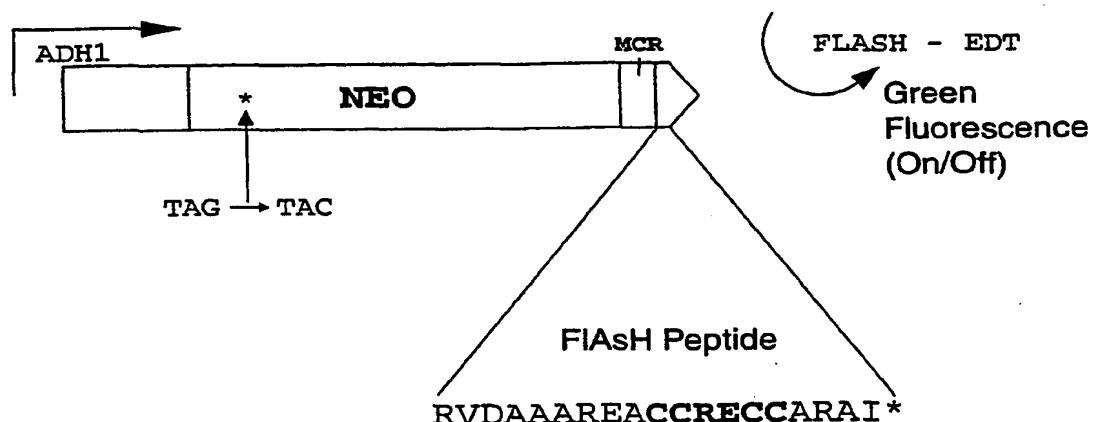


Figure 9

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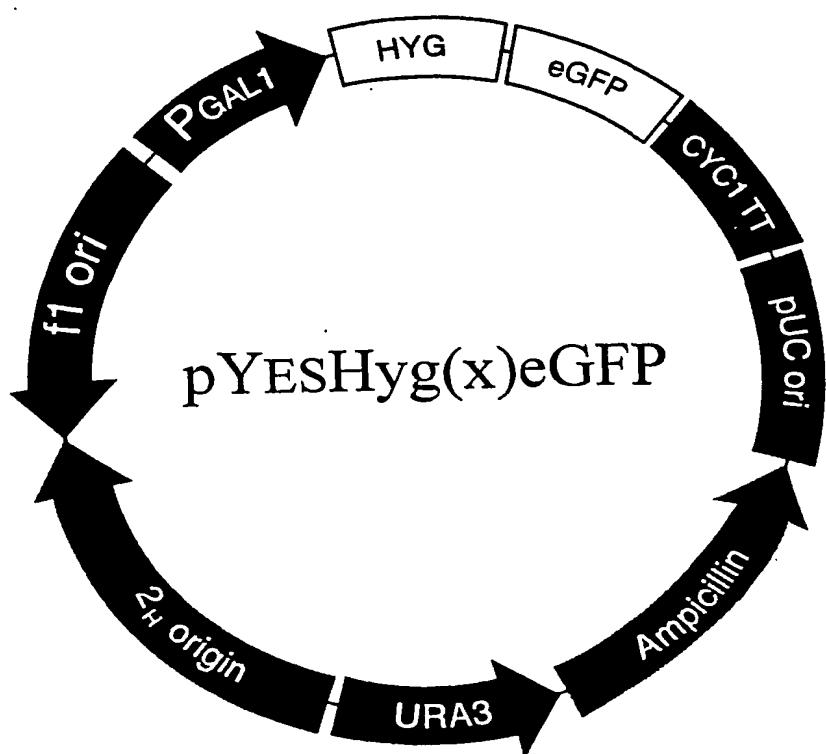


Figure 10

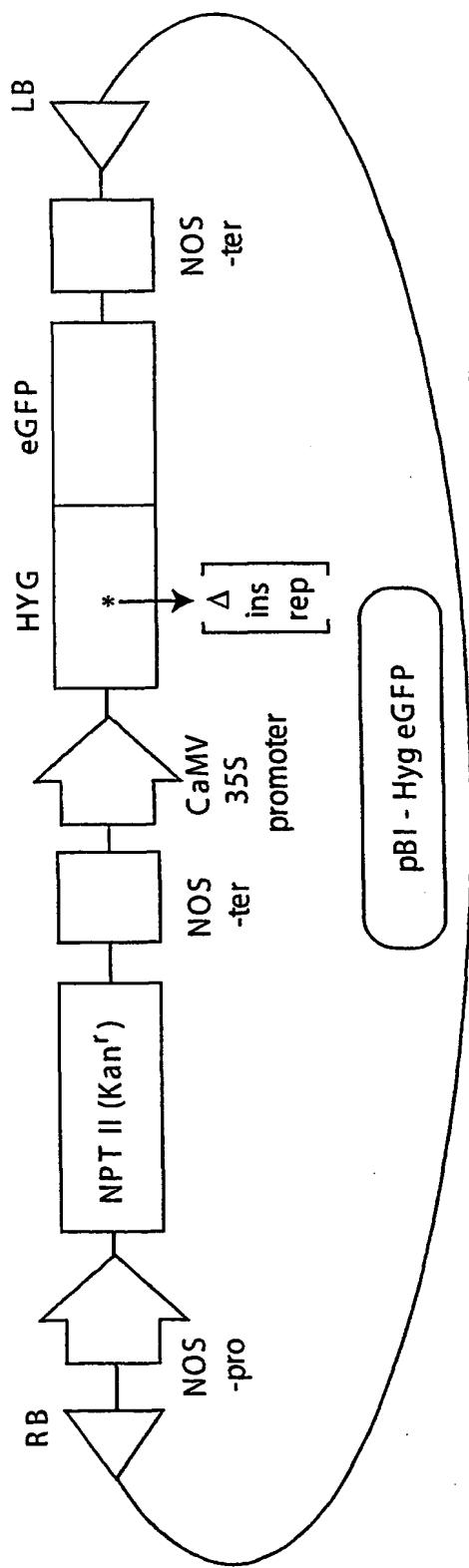


Figure 11

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(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
6 December 2001 (06.12.2001)

PCT

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A01H 5/00

PA 18940 (US). KIM, Jungsup [KR/US]; 3 Chase Hall,  
Newark, DE 19711 (US).

(21) International Application Number: PCT/US01/17672

(74) Agents: HALEY, James, F., Jr. et al.; Fish & Neave, 1251  
Avenue of the Americas, New York, NY 10020 (US).

(22) International Filing Date: 1 June 2001 (01.06.2001)

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CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,  
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,  
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ZW.

(25) Filing Language: English

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patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
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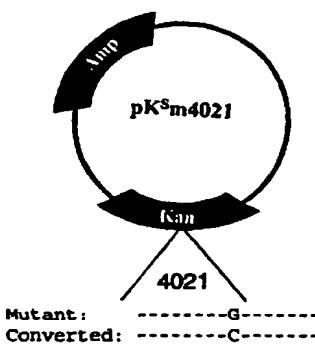
— as to applicant's entitlement to apply for and be granted  
a patent (Rule 4.17(ii)) for the following designations AE,  
AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA,

(71) Applicant (for all designated States except US): UNIVERSITY OF DELAWARE [US/US]; 210 Hullihen Hall, Newark, DE 19716 (US).

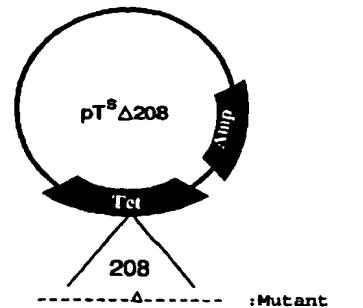
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(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

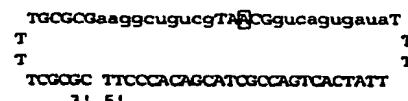
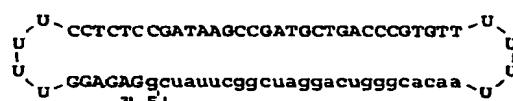
Plasmids, DNA targets and chimeric oligonucleotides



KanGG



TetΔ208T



WO 01/092512 A3

(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclease-resistant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.



CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)

— as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)

— as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,

RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)

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**Published:**

— with international search report

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9 January 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

## INTERNATIONAL SEARCH REPORT

International Application No PCT/US 01/17672
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A. CLASSIFICATION OF SUBJECT MATTER					
IPC 7	C12N15/10 C12N5/04	C12N15/82 A01H5/00	C12N15/11	C07H21/04	A61K31/7088

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7	C12N
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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, SEQUENCE SEARCH
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## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WOOLF T M ET AL: "TOWARD THE THERAPEUTIC EDITING OF MUTATED RNA SEQUENCES" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 92, 1 August 1995 (1995-08-01), pages 8298-8302, XP000574995 ISSN: 0027-8424 the whole document	1-3,5,8, 9,12-14, 17,20
Y	---	1-6, 8-12,17, 18,20

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

## \* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

22 March 2002

Date of mailing of the international search report

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## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 01/17672

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GAMPER HOWARD B JR ET AL: "A plausible mechanism for gene correction by chimeric oligonucleotides." BIOCHEMISTRY, vol. 39, no. 19, 16 May 2000 (2000-05-16), pages 5808-5816, XP002192327 ISSN: 0006-2960 cited in the application the whole document ---	13-16
Y	---	1-6,8-12
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A	WO 99 07865 A (KIMERAGEN INC) 18 February 1999 (1999-02-18) cited in the application the whole document ---	1-6,8-20
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A	WO 99 14226 A (WENGEL JESPER ;EXIQON A S (DK); NIELSEN POUL (DK)) 25 March 1999 (1999-03-25) page 56, line 16 - line 30 page 149; example 131 page 168 -page 173; examples 151,152 claims 93-108 ---	1-4
P,X	GAMPER HOWARD B ET AL: "The DNA strand of chimeric RNA/DNA oligonucleotides can direct gene repair/conversion activity in mammalian and plant cell-free extracts." NUCLEIC ACIDS RESEARCH, vol. 28, no. 21, 1 November 2000 (2000-11-01), pages 4332-4339, XP002192329 ISSN: 0305-1048 the whole document ---	1-6,8-16
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		-/-

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/17672

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	WO 01 24615 A (VALIGEN US INC) 12 April 2001 (2001-04-12) the whole document ---	1-20
E	WO 01 73002 A (UNIV DELAWARE ;GAMPER HOWARD B (US); KMIEC ERIC B (US); RICE MICHA) 4 October 2001 (2001-10-04) the whole document ---	1-6,8-20
T	RICE MICHAEL C ET AL: "The potential of nucleic acid repair in functional genomics." NATURE BIOTECHNOLOGY, vol. 19, no. 4, April 2001 (2001-04), pages 321-326, XP002192330 ISSN: 1087-0156 ---	
T	KMIEC ERIC B ET AL: "Chloroplast lysates support directed mutagenesis via modified DNA and chimeric RNA/DNA oligonucleotides." PLANT JOURNAL, vol. 27, no. 3, August 2001 (2001-08), pages 267-274, XP002192584 ISSN: 0960-7412 -----	

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 01/17672

### Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:  
Although claims 8,10,12 (as far as in vivo methods) are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2.  Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3.  Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-20 (all partially)

#### Remark on Protest

The additional search fees were accompanied by the applicant's protest.  
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. : Claims 1-20 (all partially)

Oligonucleotides characterised by SEQ IDs 4341-4344 for targeted alteration of the *Arabidopsis EPSPS* at aminoacid position 97; modified forms thereof; compositions and kits comprising them; methods for their optimisation.

Inventions 2. to 668. : Claims 1-20 (all partially)

As for subject 1., but concerning respectively the 667 groups of altering oligonucleotides (SEQ IDs 4345-7012) for each individual mutation disclosed in Tables 10 to 24.

## INTERNATIONAL SEARCH REPORT

## Information on patent family members

International Application No

PCT/US 01/17672

Patent document cited in search report	Publication date		Patent family member(s)	Publication date
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